

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 27, 2005, 07:32:56 ; Search time 215.886 Seconds
(without alignments)
1479.779 Million cell updates/sec

Title: US-09-922-958-4
Perfect score: 4287
Sequence: 1 MEGAGGANDKKKISSERRKE.....QGSRNLLQGEELLRALDQVN 826

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	4287	100.0	826	2	AAU06289	Aay06289 Human tra
4	4287	100.0	826	3	AAU69407	Aay69407 A wild ty
5	4287	100.0	826	3	AAU94640	Aay94640 Human hyp
6	4287	100.0	826	4	AAB76854	Aab76854 Human lun
7	4287	100.0	826	5	AAU85509	Aau85509 Clone #19
8	4287	100.0	826	5	AAU77602	Aau77602 Human hyp
9	4287	100.0	826	5	AAE24212	Aae24212 Human HIF

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35	4282	99.9	826	5	ABP54718	Abp54718	Hypoxia i
36	4281	99.9	826	5	AAU77613	Aau77613	Human hyp
37	4279	99.8	826	5	AAU77615	Aau77615	Human hyp
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39	4279	99.8	826	5	ABP54716	Abp54716	Hypoxia i
40	4278	99.8	826	5	AAU77617	Aau77617	Human hyp
41	4278	99.8	826	6	ADA18532	Ada18532	Human hyp
42	4277	99.8	826	5	AAU77609	Aau77609	Human hyp
43	4274	99.7	826	5	AAU77611	Aau77611	Human hyp
44	4274	99.7	826	5	ABP54719	Abp54719	Hypoxia i
45	4273.5	99.7	827	7	ADE25733	Ade25733	Human pro

ALIGNMENTS

RESULT 1

AAW06557

ID AAW06557 standard; protein; 826 AA.

XX

AC AAW06557;

XX

DT 19-MAR-1997 (first entry)

XX

DE Human hypoxia inducible factor-1 alpha.

XX

KW Hypoxia inducible factor-1 alpha; HIF-1; tissue damage; atherosclerosis;

KW cerebral artery disease; therapy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 17. .30
 FT /label= DNA-binding_domain
 FT /note= "the DNA binding domain is deleted in engineered
 FT HIF-1 alpha variants"
 XX
 PN WO9639426-A1.
 XX
 PD 12-DEC-1996.
 XX
 PF 06-JUN-1996; 96WO-US010251.
 XX
 PR 06-JUN-1995; 95US-00480473.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MED.
 XX
 PI Semenza GL;
 XX
 DR WPI; 1997-043061/04.
 DR N-PSDB; AAT45937.
 XX
 PT DNA encoding human hypoxia-inducible factor 1 alpha - useful for
 PT enhancing expression of structural gene and treatment of hypoxia-related
 PT tissue damage.
 XX
 PS Disclosure; Page 49-53; 95pp; English.
 XX
 CC The 120 kDa alpha subunit (AAW06557) of human hypoxia inducible factor-1
 CC (HIF-1) is a basic-helix-loop-helix polypeptide contg. a PAS domain whose
 CC expression is regulated by cellular O2 tension. It dimerises with a beta
 CC subunit to form HIF-1, a DNA-binding protein which binds to the enhancer
 CC region of e.g. erythropoietin and vascular endothelial growth factor
 CC genes. Its amino acid sequence was deduced from cDNA clones (see also
 CC AAT45937) obtd. from an Hep3B library. Recombinant HIF-1 alpha can be
 CC produced in transformed host cells and used to treat HIF-1-mediated or
 CC hypoxia- related disorders. Dominant-negative variant forms (see also
 CC AAW06558-59) of HIF-1 alpha have been engineered that form a
 CC nonfunctional HIF-1 complex
 XX
 SQ Sequence 826 AA;

Query Match 100.0%; Score 4287; DB 2; Length 826;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 826; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEGAGGANDKKKISSERRKEKSRDAARRSRSESEVIFYELAHQLPLPHNVSSHLDKASVM 60
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 Qy 61 RLTISYLRVRKLLDAGDLIEDDMKAQMNCFYLKALDGFVMVLTDDGDMIYISDNVNKYM 120
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 Db 61 RLTISYLRVRKLLDAGDLIEDDMKAQMNCFYLKALDGFVMVLTDDGDMIYISDNVNKYM 120
 Qy 121 GLTQFELTGHSVFDFTTHPCDHEEMREMLTHRNLVKKGKEQNTQRSFFLRMKCTLTSRGR 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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 Qy 181 TMNIKSATWKVLHCTGHIHVYDTNSNPQCGYKKPPMTCLVLICEPIPHPSNIEIPLDSK 240

Db	181		TMNIKSATWKVLHCTGHIHVYDTNSNQPCGYKKPPMTCLVLICEPIPHPSNIEIPLDSK	240
Qy	241		TFLSRHSLDMKFSYCDERITELMGYEPEELLGRSIYEYHALDSHDHLTKTHHDMFTKGQV	300
Db	241		TFLSRHSLDMKFSYCDERITELMGYEPEELLGRSIYEYHALDSHDHLTKTHHDMFTKGQV	300
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Db	301		TTGQYRMLAKRGGYVWVETQATVIYNTKNSQPQCIVCVNYVVGIIQHDLIFSLQQTECV	360
Qy	361		LKPVESSDMKMTQLFTKVESEDTSFLDKLKKEPDALTLLAPAAGDTIISLDFGSNDTET	420
Db	361		LKPVESSDMKMTQLFTKVESEDTSFLDKLKKEPDALTLLAPAAGDTIISLDFGSNDTET	420
Qy	421		DDQQLEEVPLYNDVMLPSPNEKLQNINLAMSPLETAETPKPLRSSADPALNQEVALKLEP	480
Db	421		DDQQLEEVPLYNDVMLPSPNEKLQNINLAMSPLETAETPKPLRSSADPALNQEVALKLEP	480
Qy	481		NPESLELSFTMPQIQDQTPSPSDGSTROSSPEPNPSEYCFYVDSMDVNEFKLELVEKLF	540
Db	481		NPESLELSFTMPQIQDQTPSPSDGSTROSSPEPNPSEYCFYVDSMDVNEFKLELVEKLF	540
Qy	541		AEDTEAKNPFSTQDSDLLEMLAPYIPMDDDFQLRSFDQLSPLESSSASPESASPQSTVT	600
Db	541		AEDTEAKNPFSTQDSDLLEMLAPYIPMDDDFQLRSFDQLSPLESSSASPESASPQSTVT	600
Qy	601		VFQQTQIQEPTANATTTTATDELKTVTKDRMEDIKILIASPSPTHIHKETTSATSSPYR	660
Db	601		VFQQTQIQEPTANATTTTATDELKTVTKDRMEDIKILIASPSPTHIHKETTSATSSPYR	660
Qy	661		DTQSRTASPNRAGKGVIEQTEKSHPRSPNVLSVALSQRTTVPEEELNPKILALQNAQRKR	720
Db	661		DTQSRTASPNRAGKGVIEQTEKSHPRSPNVLSVALSQRTTVPEEELNPKILALQNAQRKR	720
Qy	721		KMEHDGSLFQAVGIGTLLQQPDDHAATTSLSWKRVGCKSSEQNGMEQKTIILIPSDLAC	780
Db	721		KMEHDGSLFQAVGIGTLLQQPDDHAATTSLSWKRVGCKSSEQNGMEQKTIILIPSDLAC	780
Qy	781		RLLGQSMDESGLPQLTSYDCEVNAPIQGSRNLLQGEELLRALDQVN	826
Db	781		RLLGQSMDESGLPQLTSYDCEVNAPIQGSRNLLQGEELLRALDQVN	826

RESULT 2

AAW80418

ID AAW80418 standard; protein; 826 AA.

XX

AC AAW80418;

XX

DT 14-JAN-1999 (first entry)

XX

DE Amino acid sequence of human hypoxia inducible factor 1 alpha.

XX

KW Human transforming growth factor-beta 3; TGF-beta3; oxygen tension;

KW trophoblast invasion regulation; inhibitor; HIF-1 alpha;

KW TGF-beta family cytokine receptor; hypoxia inducible factor 1 alpha;

KW preeclampsia; pregnancy; choriocarcinoma; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9840747-A1.
 XX
 PD 17-SEP-1998.
 XX
 PF 05-MAR-1998; 98WO-CA000180.
 XX
 PR 07-MAR-1997; 97US-0039919P.
 XX
 PA (MOUN) MOUNT SINAI HOSPITAL CORP.
 PA (HOSP-) HOSPITAL FOR SICK CHILDREN.
 XX
 PI Caniggia I, Post M, Lye S;
 XX
 DR WPI; 1998-520837/44.
 DR N-PSDB; AAV63210.
 XX
 PT Regulation of trophoblast invasion - by, e.g. transforming growth factor-
 PT beta3 inhibitor, useful for detecting or treating preeclampsia in
 PT pregnant women.
 XX
 PS Disclosure; Fig 2; 59pp; English.
 XX
 CC The present sequence encodes human hypoxia inducible factor 1 alpha (HIF-
 CC 1 alpha). The specification describes a composition for regulating
 CC trophoblast invasion which comprises an inhibitor of transforming growth
 CC factor-beta 3 (TGF-beta3), TGF-beta family cytokine receptors, HIF-1
 CC alpha or oxygen tension. The composition is used in methods of
 CC diagnosing, monitoring, preventing or treating conditions requiring
 CC regulation of trophoblast invasion, especially preeclampsia in pregnant
 CC women or choriocarcinomas
 XX
 SQ Sequence 826 AA;

Query Match 100.0%; Score 4287; DB 2; Length 826;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 826; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEGAGGANDKKKISSERRKEKSRDAARSRRSKESEVIFYELAHQLPLPHNVSSHLDKASVM 60
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 Db 1 MEGAGGANDKKKISSERRKEKSRDAARSRRSKESEVIFYELAHQLPLPHNVSSHLDKASVM 60
 Qy 61 RLTISYLRVRKLLDAGDLIEDDMKAQMNCFYLKALDGFVMVLTDDGDMIYISDNVNKYM 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 RLTISYLRVRKLLDAGDLIEDDMKAQMNCFYLKALDGFVMVLTDDGDMIYISDNVNKYM 120
 Qy 121 GLTQFELTGHSVDFDTHPCDHEEMREMLTHRNLVKKGKEQNTQRSFFLRMKCTLT SRGR 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 GLTQFELTGHSVDFDTHPCDHEEMREMLTHRNLVKKGKEQNTQRSFFLRMKCTLT SRGR 180
 Qy 181 TMNIKSATWKVLHCTGHIHVYDTNSNPQCGYKKPPMTCLVLICEPIPHPSNIEIPLDSK 240
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 Db 181 TMNIKSATWKVLHCTGHIHVYDTNSNPQCGYKKPPMTCLVLICEPIPHPSNIEIPLDSK 240

Qy	241	TFLSRHSLDMKFSYCDERITELMGYEPEELLGRSIYEYYHALDSDHCLKTHHDMFTKGQV	300
Db	241	TFLSRHSLDMKFSYCDERITELMGYEPEELLGRSIYEYYHALDSDHCLKTHHDMFTKGQV	300
Qy	301	TTGQYRMLAKRGGYVWVETQATVIYNTKNSQPQCIVCVNYVVSIGIIQHDLIFSLQQTECV	360
Db	301	TTGQYRMLAKRGGYVWVETQATVIYNTKNSQPQCIVCVNYVVSIGIIQHDLIFSLQQTECV	360
Qy	361	LKPVESSDMKMTQLFTKVESEDTSLSFDKLKKEPDALTLLAPAAGDTIISLDFGSNDTET	420
Db	361	LKPVESSDMKMTQLFTKVESEDTSLSFDKLKKEPDALTLLAPAAGDTIISLDFGSNDTET	420
Qy	421	DDQQLEEVPLYNDVMLPSPNEKLQNINLAMSPLPATETPKPLRSSADPALNQEVALKLEP	480
Db	421	DDQQLEEVPLYNDVMLPSPNEKLQNINLAMSPLPATETPKPLRSSADPALNQEVALKLEP	480
Qy	481	NPESLELSFTMPQIQDQTPSPSDGSTRQSSPEPNPSEYCFYVDSMDVNEFKLELVEKLF	540
Db	481	NPESLELSFTMPQIQDQTPSPSDGSTRQSSPEPNPSEYCFYVDSMDVNEFKLELVEKLF	540
Qy	541	AEDTEAKNPFSTQDSDLLEMLAPYIPMDDDFQLRSFDQLSPLESSSASPESASPQSTVT	600
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Qy	601	VFQQTQIQEPTANATTTTATTDDELKTVTKDRMEDIKILIASPSPTHIHKETTSATSSPYR	660
Db	601	VFQQTQIQEPTANATTTTATTDDELKTVTKDRMEDIKILIASPSPTHIHKETTSATSSPYR	660
Qy	661	DTQSRTASPNRAGKGVIEQTEKSHPRSPNVLSVALSQRTTVPEEELNPKILALQNAQRKR	720
Db	661	DTQSRTASPNRAGKGVIEQTEKSHPRSPNVLSVALSQRTTVPEEELNPKILALQNAQRKR	720
Qy	721	KMEHDGSLFQAVGIGTLLQQPDDHAATTSLSWKRVKGCKSSEQNGMEQKTIILIPSDLAC	780
Db	721	KMEHDGSLFQAVGIGTLLQQPDDHAATTSLSWKRVKGCKSSEQNGMEQKTIILIPSDLAC	780
Qy	781	RLQGQSMDESGLPQLTSYDCEVNAPIQGSRNLLQGEELLRALDQVN	826
Db	781	RLQGQSMDESGLPQLTSYDCEVNAPIQGSRNLLQGEELLRALDQVN	826

us-09-922-958-4.rapb

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OM protein - protein search, using sw model

Run on: July 27, 2005, 07:53:38 ; Search time 203.684 Seconds
(without alignments)
1577.480 Million cell updates/sec

Title: US-09-922-958-4
Perfect score: 4287
Sequence: 1 MEGAGGANDKKKISSERRKE.....QGSRNLLQGEELLRALDQVN 826

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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5	4287	100.0	826	9	US-09-849-626-330	Sequence 330, App
6	4287	100.0	826	10	US-09-967-388-4	Sequence 4, Appli
7	4287	100.0	826	10	US-09-476-300-330	Sequence 330, App
8	4287	100.0	826	13	US-10-028-158-23	Sequence 23, Appl
9	4287	100.0	826	13	US-10-101-812-10	Sequence 10, Appl
10	4287	100.0	826	14	US-10-101-662A-9	Sequence 9, Appli
11	4287	100.0	826	14	US-10-017-754-330	Sequence 330, App
12	4287	100.0	826	14	US-10-115-987B-14	Sequence 14, Appl
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14	4287	100.0	826	14	US-10-113-872-330	Sequence 330, App
15	4287	100.0	826	14	US-10-423-419-2	Sequence 2, Appli
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17	4287	100.0	826	16	US-10-032-361-1	Sequence 1, Appli
18	4287	100.0	826	16	US-10-859-935-10	Sequence 10, Appl
19	4287	100.0	826	16	US-10-859-935-23	Sequence 23, Appl
20	4287	100.0	826	17	US-10-901-583-18	Sequence 18, Appl
21	4287	100.0	826	18	US-10-472-595A-35	Sequence 35, Appl
22	4287	100.0	826	20	US-11-043-493-23	Sequence 23, Appl
23	4282	99.9	826	14	US-10-101-816-5	Sequence 5, Appli
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25	4279	99.8	826	14	US-10-101-816-2	Sequence 2, Appli
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35	3797	88.6	836	18	US-10-988-486-6	Sequence 6, Appli
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37	2716	63.4	542	15	US-10-264-049-2606	Sequence 2606, Ap
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39	1735.5	40.5	870	14	US-10-101-816-4	Sequence 4, Appli
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42	1182.5	27.6	632	15	US-10-425-833-10	Sequence 10, Appl
43	1132.5	26.4	705	14	US-10-154-386-2	Sequence 2, Appli
44	1104	25.8	595	15	US-10-425-833-7	Sequence 7, Appli
45	906	21.1	333	9	US-09-925-302-659	Sequence 659, App

ALIGNMENTS

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RESULT 1
US-09-922-958-4
; Sequence 4, Application US/09922958
; Patent No. US20020048794A1
; GENERAL INFORMATION:
; APPLICANT: POELLINGER, Lorenz
; APPLICANT: PEREIRA, Teresa
; APPLICANT: RUAS, Jorge
; TITLE OF INVENTION: MECHANISM OF CONDITIONAL REGULATION OF THE HYPOXIA-INDUCIBLE
FACTOR-1 BY
; TITLE OF INVENTION: THE VON HIPPEL-LINDAU TUMOR SUPPRESSOR PROTEIN
; FILE REFERENCE: 3743/49008
; CURRENT APPLICATION NUMBER: US/09/922,958
; CURRENT FILING DATE: 2001-08-07

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; PRIOR APPLICATION NUMBER: US 60/223,480
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-958-4

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Query Match      100.0%; Score 4287; DB 9; Length 826;
Best Local Similarity 100.0%; Pred. No. 3.1e-289;
Matches 826; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEGAGGANDKKKISSERRKEKSRDAARRSRSESEVFYELAHQLPLPHNVSSHLDKASVM 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEGAGGANDKKKISSERRKEKSRDAARRSRSESEVFYELAHQLPLPHNVSSHLDKASVM 60

Qy     61 RL TISYLRVRKLLDAGDLIEDDMKAQMNC FYLKALDGFVMVL TDDGDMIYISDNVNKYM 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 RL TISYLRVRKLLDAGDLIEDDMKAQMNC FYLKALDGFVMVL TDDGDMIYISDNVNKYM 120

Qy    121 GL TQFELTGHSVDFDTHPCDHEEMREML THRNGLVKKGKEQNTQRSFFLRMKCTLTSRGR 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GL TQFELTGHSVDFDTHPCDHEEMREML THRNGLVKKGKEQNTQRSFFLRMKCTLTSRGR 180

Qy    181 TMNIKSATWKVLHCTGHIHVYDTNSNPQCGYKKPPMTCLVLICEPIPHPSNIEIPLDSK 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TMNIKSATWKVLHCTGHIHVYDTNSNPQCGYKKPPMTCLVLICEPIPHPSNIEIPLDSK 240

Qy    241 TFLSRHSLDMKFSYCDERITELMGYEPEELLGRSIEYYHALDSHDLTKTHHDMFTKGQV 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TFLSRHSLDMKFSYCDERITELMGYEPEELLGRSIEYYHALDSHDLTKTHHDMFTKGQV 300

Qy    301 TTGQYRMLAKRGGYVWVETQATVIYNTKNSQPQCIVCVNYVSGIIQHDLIFSLQQTECV 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TTGQYRMLAKRGGYVWVETQATVIYNTKNSQPQCIVCVNYVSGIIQHDLIFSLQQTECV 360

Qy    361 LKPVESSDMKMTQLFTKVESED TSSLFDKLKKEPDALTLLAPAAGDTIISLDFGSNDTET 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 LKPVESSDMKMTQLFTKVESED TSSLFDKLKKEPDALTLLAPAAGDTIISLDFGSNDTET 420

Qy    421 DDQQL EEVPLYNDVMLPSPNEKLQINLAMSP LPTAETPKPLRSSADPALNQEVALKLEP 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 DDQQL EEVPLYNDVMLPSPNEKLQINLAMSP LPTAETPKPLRSSADPALNQEVALKLEP 480

Qy    481 NPESLELSFTMPQIQDQTPSPSDGSTRQSSPEPNSPSEYCFYVDSMDVNEFKLELVEKLF 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 NPESLELSFTMPQIQDQTPSPSDGSTRQSSPEPNSPSEYCFYVDSMDVNEFKLELVEKLF 540

Qy    541 AEDTEAKNPFSTQD TDL DLEMLAPYIPMDDDFQLRSFDQLSPLESSSASPESASPQSTVT 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 AEDTEAKNPFSTQD TDL DLEMLAPYIPMDDDFQLRSFDQLSPLESSSASPESASPQSTVT 600

Qy    601 VFQQTQIQEPTANATTTTATTD ELKTVTKDRMEDIKILIASPSPTHIHKETTSATSSPYR 660
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 VFQQTQIQEPTANATTTTATTD ELKTVTKDRMEDIKILIASPSPTHIHKETTSATSSPYR 660

Qy    661 DTQSRTASPNRAGKGVIEQTEKSHRSPNVL SVALSQRTTVPEEELNPKILALQNAQRKR 720
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 DTQSRTASPNRAGKGVIEQTEKSHRSPNVL SVALSQRTTVPEEELNPKILALQNAQRKR 720

Qy    721 KMEHDGSLFQAVGIGTLLQQPDDHAATTSLSWKRVGCKSSEQNGMEQKTIILIPSDLAC 780

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                                us-09-922-958-4.rapb
Db      721 |||||KMEHDGSLFQAVGIGTLLQQPDDHAATTSLSWKRVKGCKSSEQNGMEQKTIILIPSDLAC 780
Qy      781 RLLGQSMDESGLPQLTSYDCEVNAPIQGSRNLLQGEELLRALDQVN 826
Db      781 |||||RLLGQSMDESGLPQLTSYDCEVNAPIQGSRNLLQGEELLRALDQVN 826

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RESULT 2

US-09-833-790-235

; Sequence 235, Application US/09833790

; Patent No. US20020068288A1

GENERAL INFORMATION:

; APPLICANT: Lodes, Michael J.

; APPLICANT: Wang, Tongtong

; APPLICANT: Secrist, Heather

; APPLICANT: Mohamath, Raodoh

; APPLICANT: Indirias, Carol Y.

; APPLICANT: Fan, Liqun

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.512

; CURRENT APPLICATION NUMBER: US/09/833,790

; CURRENT FILING DATE: 2001-04-11

; NUMBER OF SEQ ID NOS: 440

; SOFTWARE: FastSEQ for windows Version 4.0

; SEQ ID NO 235

; LENGTH: 826

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-833-790-235

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Query Match          100.0%; Score 4287; DB 9; Length 826;
Best Local Similarity 100.0%; Pred. No. 3.1e-289;
Matches 826; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEGAGGANDKKKISSERRKEKSRDAARSRRSKESEVFYELAHQLPLPHNVSSHLDKASVM 60
Db      1 MEGAGGANDKKKISSERRKEKSRDAARSRRSKESEVFYELAHQLPLPHNVSSHLDKASVM 60
Qy     61 RLTISYLRVRKLLDAGDLIEDDMKAQMNCFYLKALDGFVMVLTDGDMIYISDNVNKYM 120
Db     61 RLTISYLRVRKLLDAGDLIEDDMKAQMNCFYLKALDGFVMVLTDGDMIYISDNVNKYM 120
Qy    121 GLTQFELTGHSVDFDTHPCDHEEMREMLTHRNLVKKGKEQNTQRSFFLRMKCTLTSGR 180
Db    121 GLTQFELTGHSVDFDTHPCDHEEMREMLTHRNLVKKGKEQNTQRSFFLRMKCTLTSGR 180
Qy    181 TMNIKSATWKVLHCTGHIHVYDTNSNPQCGYKKPPMTCLVLICEPIPHPSNIEIPLDSK 240
Db    181 TMNIKSATWKVLHCTGHIHVYDTNSNPQCGYKKPPMTCLVLICEPIPHPSNIEIPLDSK 240
Qy    241 TFLSRHSLDMKFSYCDERITELMGYEPEELLGRSIEYEHYHALDSHDLTKTHHDMFTKGQV 300
Db    241 TFLSRHSLDMKFSYCDERITELMGYEPEELLGRSIEYEHYHALDSHDLTKTHHDMFTKGQV 300
Qy    301 TTGQYRMLAKRGGYVWVETQATVIYNTKNSQPQCIVCVNYVSGIIQHDLIFSLQQTECV 360
Db    301 TTGQYRMLAKRGGYVWVETQATVIYNTKNSQPQCIVCVNYVSGIIQHDLIFSLQQTECV 360
Qy    361 LKPVESSDMKMTQLFTKVESEDTSLLFDKLLKKEPDALTLLAPAAGDTIISLDFGSNDTET 420
Db    361 LKPVESSDMKMTQLFTKVESEDTSLLFDKLLKKEPDALTLLAPAAGDTIISLDFGSNDTET 420

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us-09-922-958-4.rapb

Qy	421	DDQQL EEVPLYNDVMLPSPNEKLQINLAMSPLPTAETPKPLRSSADPALNQEVALKLEP	480
Db	421	DDQQL EEVPLYNDVMLPSPNEKLQINLAMSPLPTAETPKPLRSSADPALNQEVALKLEP	480
Qy	481	NPESLELSFTMPQIQDQTPSPSDGSTRQSSPEPNPSEYCFYVDSMDVNEFKLELVEKLF	540
Db	481	NPESLELSFTMPQIQDQTPSPSDGSTRQSSPEPNPSEYCFYVDSMDVNEFKLELVEKLF	540
Qy	541	AEDTEAKNPFSTQDSDLLEMLAPYIPMDDDFQLRSFDQLSPLESSSASPESASPQSTVT	600
Db	541	AEDTEAKNPFSTQDSDLLEMLAPYIPMDDDFQLRSFDQLSPLESSSASPESASPQSTVT	600
Qy	601	VFQQTQIQEPTANATTTTATTDDELKTVTKDRMEDIKILIASPSPTHIHKETTSATSSPYR	660
Db	601	VFQQTQIQEPTANATTTTATTDDELKTVTKDRMEDIKILIASPSPTHIHKETTSATSSPYR	660
Qy	661	DTQSRTASPNRAGKGVIEQTEKSHRSPNVLSVALSQRTTVPEEELNPKILALQNAQRKR	720
Db	661	DTQSRTASPNRAGKGVIEQTEKSHRSPNVLSVALSQRTTVPEEELNPKILALQNAQRKR	720
Qy	721	KMEHDGSLFQAVGIGTLLQQPDDHAATTSLSWKRVKGCKSSEQNGMEQKTIILIPSDLAC	780
Db	721	KMEHDGSLFQAVGIGTLLQQPDDHAATTSLSWKRVKGCKSSEQNGMEQKTIILIPSDLAC	780
Qy	781	RLLGQSMDESGLPQLTSYDCEVNAPIQGSRNLLQGEELLRALDQVN	826
Db	781	RLLGQSMDESGLPQLTSYDCEVNAPIQGSRNLLQGEELLRALDQVN	826

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OM protein - protein search, using sw model

Run on: July 27, 2005, 07:42:11 ; Search time 48.8091 Seconds
(without alignments)
1628.284 Million cell updates/sec

Title: US-09-922-958-4
Perfect score: 4287
Sequence: 1 MEGAGGANDKKKISSERRKE.....QGSRNLLQGEELLRALDQVN 826

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	4287	100.0	826	2	I38972	hypoxia-inducible
2	3764.5	87.8	813	2	JC5809	hypoxia-inducible
3	3754	87.6	810	2	JC4837	hypoxia-inducible
4	3406.5	79.5	811	2	JC7619	hypoxia-inducible
5	1165.5	27.2	667	2	JC7771	hypoxia inducible
6	888.5	20.7	1505	2	JC4851	hypoxia-inducible
7	570	13.3	655	2	A29945	neurogenesis regul
8	512	11.9	823	2	T21943	hypothetical prote
9	511	11.9	825	2	T21944	hypothetical prote
10	441.5	10.3	248	2	A58520	single-minded gene
11	422	9.8	776	2	A55448	Ah receptor nuclea
12	413.5	9.6	791	2	A56241	aryl hydrocarbon r
13	397.5	9.3	626	2	JC5405	brain and muscle A

14	396	9.2	626	2	JE0270	Arnt-like PAS prot
15	396	9.2	846	2	JC7721	aryl hydrocarbon r
16	390.5	9.1	789	2	I59550	aryl hydrocarbon r
17	390.5	9.1	805	2	A46266	aryl hydrocarbon r
18	377.5	8.8	805	2	JC7635	aryl hydrocarbon r
19	370	8.6	834	2	JC7993	aryl hydrocarbon r
20	362.5	8.5	848	2	S59514	aryl hydrocarbon r
21	362.5	8.5	853	2	S58375	aryl hydrocarbon r
22	361	8.4	920	2	JC7313	aryl hydrocarbon r
23	348.5	8.1	1059	2	T30557	aryl hydrocarbon r
24	346.5	8.1	1058	2	T30556	aryl hydrocarbon r
25	338	7.9	358	2	S58376	aryl hydrocarbon r
26	338	7.9	1023	2	T13068	CLOCK protein - fr
27	336	7.8	1015	2	T13062	CLOCK protein - fr
28	329	7.7	1027	2	T13071	CLOCK protein - fr
29	315.5	7.4	392	2	JC7633	aryl hydrocarbon n
30	301	7.0	300	2	T24292	hypothetical prote
31	277	6.5	602	2	T19898	aryl hydrocarbon r
32	273.5	6.4	1462	2	T42639	glucocorticoid rec
33	269	6.3	1424	2	T03851	thyroid hormone re
34	268	6.3	647	2	T19307	hypothetical prote
35	266.5	6.2	650	2	G87883	protein C41G7.5 [i
36	250.5	5.8	451	2	T42397	aryl hydrocarbon r
37	244.5	5.7	453	2	T19440	hypothetical prote
38	231.5	5.4	1016	2	T30990	period protein - C
39	231.5	5.4	1018	2	T30986	period protein - C
40	216	5.0	1122	2	B26427	period clock prote
41	216	5.0	1127	2	A25018	circadian rhythm p
42	216	5.0	1176	2	C26427	period clock prote
43	216	5.0	1218	2	A26588	period clock prote
44	216	5.0	1218	2	A26427	period clock prote
45	215.5	5.0	1208	2	S17286	period clock prote

ALIGNMENTS

RESULT 1

I38972

hypoxia-inducible factor 1 alpha - human

N;Alternate names: ARNT interacting protein

C;Species: Homo sapiens (man)

C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004

C;Accession: I38972; G01875

R;Wang, G.L.; Jiang, B.H.; Rue, E.A.; Semenza, G.L.

Proc. Natl. Acad. Sci. U.S.A. 92, 5510-5514, 1995

A;Title: Hypoxia-inducible factor 1 is a basic-helix-loop-helix-PAS heterodimer regulated by cellular O2 tension.

A;Reference number: I38972; MUID:95296340; PMID:7539918

A;Accession: I38972

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-826 <RES>

A;Cross-references: UNIPROT:Q16665; EMBL:U22431; NID:g881345; PIDN:AAC50152.1; PID:g881346

A;Note: parts of this sequence were confirmed by peptide sequencing

R;Hogenesch, J.B.; Chan, W.K.; Carver, L.A.; Bradfield, C.A.

submitted to the EMBL Data Library, June 1995
A;Reference number: H00692
A;Accession: G01875
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-826 <HOG>
A;Cross-references: EMBL:U29165; NID:g1144012; PIDN:AAC51210.1; PID:g1144013
C;Genetics:
A;Gene: GDB:HIF1A
A;Cross-references: GDB:512229
A;Map position: 14q21-14q24
C;Keywords: heterodimer

Query Match 100.0%; Score 4287; DB 2; Length 826;
Best Local Similarity 100.0%; Pred. No. 8.2e-245;
Matches 826; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEGAGGANDKKKISSERRKEKSRDAARSRRSKESEVFYELAHQLPLPHNVSSHLDKASVM	60
Db	1	MEGAGGANDKKKISSERRKEKSRDAARSRRSKESEVFYELAHQLPLPHNVSSHLDKASVM	60
Qy	61	RLTISYLRVRKLLDAGDLIEDDMKAQMNC FYLKALDGFVMVLTDDGDMIYISDNVNKYM	120
Db	61	RLTISYLRVRKLLDAGDLIEDDMKAQMNC FYLKALDGFVMVLTDDGDMIYISDNVNKYM	120
Qy	121	GLTQFELTGHSVFDFTHPCDHEEMREMLTHRNLVKKGKEQNTQRSFFLRMKCTLTSRGR	180
Db	121	GLTQFELTGHSVFDFTHPCDHEEMREMLTHRNLVKKGKEQNTQRSFFLRMKCTLTSRGR	180
Qy	181	TMNIKSATWKVLHCTGHIHVDYDTSNQPCGYKKPPMTCLVLICEPIPHPSNIEIPLDSK	240
Db	181	TMNIKSATWKVLHCTGHIHVDYDTSNQPCGYKKPPMTCLVLICEPIPHPSNIEIPLDSK	240
Qy	241	TFLSRHSLDMKFSYCDERITELMGYEPEELLGRSIYEYHALDSHDLTKTHHDMFTKGQV	300
Db	241	TFLSRHSLDMKFSYCDERITELMGYEPEELLGRSIYEYHALDSHDLTKTHHDMFTKGQV	300
Qy	301	TTGQYRMLAKRGGYVWVETQATVIYNTKNSQPQCIVCVNYVVGIIQHDLIFSLQQTECV	360
Db	301	TTGQYRMLAKRGGYVWVETQATVIYNTKNSQPQCIVCVNYVVGIIQHDLIFSLQQTECV	360
Qy	361	LKPVESSDMKMTQLFTKVESEDTS S LFDK LKKEPDALTLLAPAAGDTIISLDFGSNDTET	420
Db	361	LKPVESSDMKMTQLFTKVESEDTS S LFDK LKKEPDALTLLAPAAGDTIISLDFGSNDTET	420
Qy	421	DDQQLEEVPLYNDVMLPSPNEKLQNINLAMSP LPTAETPKPLRSSADPALNQEVALKLEP	480
Db	421	DDQQLEEVPLYNDVMLPSPNEKLQNINLAMSP LPTAETPKPLRSSADPALNQEVALKLEP	480
Qy	481	NPESLELSFTMPQIQDQTPSPSDGSTRQSSPEPNSPSEYCFYVDSMDVNEFKLELVEKLF	540
Db	481	NPESLELSFTMPQIQDQTPSPSDGSTRQSSPEPNSPSEYCFYVDSMDVNEFKLELVEKLF	540
Qy	541	AEDTEAKNPFSTQD TDL DLEMLAPYIPMDDDFQLRSFDQLSPLESSSASPESASPQSTVT	600
Db	541	AEDTEAKNPFSTQD TDL DLEMLAPYIPMDDDFQLRSFDQLSPLESSSASPESASPQSTVT	600

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Qy      601 VFQQTQIQEPTANATTTTATTTDELKTVTKDRMEDIKILIASPSPTHIHKETTSATSSPYR 660
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 VFQQTQIQEPTANATTTTATTTDELKTVTKDRMEDIKILIASPSPTHIHKETTSATSSPYR 660

Qy      661 DTQSRTASPNRAGKGVIEQTEKSHPRSPNVLSVALSQRTTVPEEELNPKILALQNAQRKR 720
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 DTQSRTASPNRAGKGVIEQTEKSHPRSPNVLSVALSQRTTVPEEELNPKILALQNAQRKR 720

Qy      721 KMEHDGSLFQAVGIGTLLQQPDDHAATTSLSWKRVKGCKSSEQNGMEQKTIILIPSDLAC 780
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 KMEHDGSLFQAVGIGTLLQQPDDHAATTSLSWKRVKGCKSSEQNGMEQKTIILIPSDLAC 780

Qy      781 RLLGQSMDESGLPQLTSYDCEVNAPIQGSRNLLQGEELLRALDQVN 826
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 RLLGQSMDESGLPQLTSYDCEVNAPIQGSRNLLQGEELLRALDQVN 826

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RESULT 2

JC5809

hypoxia-inducible factor 1 alpha - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 26-Aug-1999

C;Accession: JC5809

R;Ladoux, A.; Frelin, C.

Biochem. Biophys. Res. Commun. 240, 552-556, 1997

A;Title: Cardiac expressions of HIF-1 alpha and HLF/EPAS, two basic loop helix/PAS domain transcription factors involved in adaptative responses to hypoxic stresses.

A;Reference number: JC5809; MUID:98063274; PMID:9398602

A;Accession: JC5809

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-813 <LAD>

C;Comment: This protein associates to the aryl hydrocarbon receptor nuclear translocator, binds to specific hypoxia responsive elements and activates the transcription of hypoxia sensitive genes such as erythropoietin, vascular endothelial growth factor, the GLUT1 glucose transporter, enzymes of glycolysis and the inducible form of nitric oxide synthase.

F;6-144/Region: basic helix-loop-helix #status predicted

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Query Match          87.8%; Score 3764.5; DB 2; Length 813;
Best Local Similarity 90.1%; Pred. No. 4.9e-214;
Matches 737; Conservative 24; Mismatches 48; Indels 9; Gaps 4;

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Qy      13 ISSERRKEKSRDAARSRRSKESEVFYELAHQLPLPHNVSSHLDKASVMRLTISYLRVRKL 72
      :||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  MSSERRKEKSRDAARSRRSKESEVFYELAHQLPLPHNVSSHLDKASVMRLTISYLRVRKL 60

Qy      73 LDAGDLIEDDMKAQMNCFYLKALDGFVMVLTDGDMIYISDNVNKYMGLTQFELTGHSV 132
      ||||||||:||||||||||||||||||||||||||||||||||||||||||
Db      61 LDAGDLIEDDMKAQMNCFYLKALDGFVMVLTDGDMIYISDNVNKYMGLTQFELTGHSV 120

Qy     133 FDFTHPCDHEEMREMLTHRNLVKKKGKEQNTQRSFFLRMKCTLTSGRGTMNISATWKVL 192
      |||||||||:||||||||||||||||||||||||||||||||||||||
Db     121 FDFTHPCDHEEMREMLTHRNGPVRKGKEQNTQRSFFLRMKCTLTSGRGTMNISATWKVL 180

Qy     193 HCTGHIHVYDTNSNQPCGYKKPPMTCLVLICEPIPHPSNIEIPLDSKTFLSRHS LDMKF 252

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Db	181	:	HCTGHIHVYDTSSNQPCGYKKPPMTCLVLICEPIPHPSNIEIPLDSKTFLSRHS LDMKF	240
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Db	241		SYCDERITELMGYEPEELLGRSIYEYHALDS DHLT KTHHDMFTKGQVTTGQYRMLAKRG	300
Qy	313		GYVWVETQATVIYNTKNSQPQCIVCVNYVVS GIIQHDLIFSLQQTECVLKPVESSDMKMT	372
Db	301		GYVWVETQATVIYNTKNSQPQCIVCVNYVVS GIIQHDLIFSLQQTESVLKPVESSDMKMT	360
Qy	373		QLFTKVESEDTS SFLDKLKKEPDALTLLAPAAGDTIIISLDFGSNDTETDDQQLEEVPLYN	432
Db	361		QLFTKVESEDTSCLFDKLKKEPDALTLLAPAAGDTIIISLDFGSDDTETEDQQLEDVPLYN	420
Qy	433		DVMLPSPNEKLQNINLAMSP LPTAETPKPLRSSADPALNQEVALKLEPNPESLELSFTMP	492
Db	421		DVMFPSSNEKL-NINLAMSP LPAETPKPLRSSADPALNQEVALKLESSPESLGLSFTMP	479
Qy	493		QIQDQTPSPSDGSTRQSSPEPNSPSEYCFYVDS DMVNEFKLELVEKLFAEDTEAKNPFST	552
Db	480		QIQDQPASPSDGSTRQSSPEPNSPSEYCFD VDS DMVNVFKLELVEKLFAEDTEAKNPFSA	539
Qy	553		QD TDL DLEMLAPYI PMDDDFQLRSFDQLSPLESSSASPESASPQSTVTVFQQTQIQEPTA	612
Db	540		QD TDL DLEMLAPYI PMDDDFQLRSFDQLSPLESNSPSPPSV---STVTGFQQTQLQKPTI	596
Qy	613		NAT-----TTTATTDELKTVTKDRMEDIKILIASPSPTHIHKETT SATSSPYRDTQSRTAS	668
Db	597		TVTAATATTATTTDESKAVTKDNIEDIKILIASPPSTQVPQEMTTAKASAYSGTHSRTAS	656
Qy	669		PNRAGKGVIEQTEKSHPRSPNVLSVALSQRTTVPEEELNPKILALQNAQRKRKMEHDGSL	728
Db	657		PDRAGKRVIEKTDKAHPRSLN-LSVTLNQRNTVPEEELNPKTIALQNAQRKRKMEHDGSL	715
Qy	729		FQAVGIGTLLQQPDDHAATTSLSWKRVKGCKSS EQNGMEQKTIILIPSDLACRLLGQSM D	788
Db	716		FQAAGIGTLLQQPGDRAPTMSLSWKRVKGYISSEQDGMEQKTI FLIPSDLACRLLGQSM D	775
Qy	789		ESGLPQLTSYDCEVNAPIQGSRNLLQGEELLRALDQVN	826
Db	776		ESGLPQLTSYDCEVNAPIQGSRNLLQGEELLRALDQVN	813

us-09-922-958-4.rup

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OM protein - protein search, using sw model

Run on: July 27, 2005, 07:33:41 ; Search time 213.07 Seconds
(without alignments)
1985.153 Million cell updates/sec

Title: US-09-922-958-4
Perfect score: 4287
Sequence: 1 MEGAGGANDKKKISSERRKE.....QGSRNLLQGEELLRALDQVN 826

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4287	100.0	826	1	HIFA_HUMAN	Q16665 homo sapien
2	4065.5	94.8	823	2	Q6IV47	Q6iv47 bos mutus g
3	4061.5	94.7	823	1	HIFA_BOVIN	Q9xta5 bos taurus
4	4017.5	93.7	821	2	Q64F54	Q64f54 spermophilu
5	3950	92.1	824	2	Q6H8T3	Q6h8t3 spalax juda
6	3941.5	91.9	819	2	Q7YSE5	Q7yse5 oryctolagus
7	3857.5	90.0	786	2	Q6SLL1	Q6sll1 canis famil
8	3803.5	88.7	825	1	HIFA_RAT	O35800 rattus norv
9	3803	88.7	836	1	HIFA_MOUSE	Q61221 mus musculu
10	3404.5	79.4	811	1	HIFA_CHICK	Q9yib9 gallus gall
11	2925	68.2	802	2	Q6PI54	Q6pi54 xenopus lae
12	2532.5	59.1	805	1	HIFA_XENLA	Q9i8a9 xenopus lae
13	2334.5	54.5	774	2	Q6STN7	Q6stn7 ctenopharyn
14	2331	54.4	777	2	Q6EHI4	Q6ehi4 brachydanio
15	2076	48.4	766	1	HIFA_ONCMY	Q98sw2 oncorhynchu
16	1962	45.8	489	2	Q6EMI3	Q6emi3 xenopus lae
17	1845	43.0	867	2	Q9W7C6	Q9w7c6 gallus gall
18	1831.5	42.7	870	2	Q9PTB3	Q9ptb3 coturnix co
19	1800.5	42.0	862	2	Q6GL61	Q6gl61 xenopus tro
20	1787	41.7	859	2	Q6GQ12	Q6gq12 xenopus lae
21	1784.5	41.6	862	2	Q6GP97	Q6gp97 xenopus lae

					us-09-922-958-4.rup	
22	1770	41.3	873	2	Q8QGM4	Q8qgm4 fundulus he
23	1765.5	41.2	870	1	PAS1_HUMAN	Q99814 homo sapien
24	1763	41.1	835	2	Q696W2	Q696w2 ctenopharyn
25	1730.5	40.4	870	2	Q9XTA4	Q9xta4 bos taurus
26	1730.5	40.4	874	1	PAS1_MOUSE	P97481 mus musculu
27	1728.5	40.3	874	2	Q6PEU2	Q6peu2 mus musculu
28	1713.5	40.0	533	2	Q6PI33	Q6pi33 brachydanio
29	1705.5	39.8	874	1	PAS1_RAT	Q9jhs1 rattus norv
30	1241	28.9	626	2	Q6EGR9	Q6egr9 brachydanio
31	1237	28.9	643	2	Q6STN6	Q6stn6 ctenopharyn
32	1171.5	27.3	662	2	Q9JHS2	Q9jhs2 rattus norv
33	1166.5	27.2	632	2	Q8WXA1	Q8wxa1 homo sapien
34	1166.5	27.2	669	2	Q66K72	Q66k72 homo sapien
35	1165.5	27.2	667	2	Q9Y2N7	Q9y2n7 homo sapien
36	1161.5	27.1	662	2	Q9Z2I5	Q9z2i5 mus musculu
37	1157	27.0	630	2	Q9QX54	Q9qx54 mus musculu
38	1156.5	27.0	632	2	Q96K34	Q96k34 homo sapien
39	1071	25.0	571	2	Q7T2E4	Q7t2e4 brachydanio
40	1004.5	23.4	1057	2	Q6DN44	Q6dn44 palaemonete
41	1002	23.4	189	2	Q6RYC8	Q6ryc8 ovis aries
42	1001.5	23.4	648	2	Q9HAI2	Q9hai2 homo sapien
43	989	23.1	189	2	Q6RYC9	Q6ryc9 sus scrofa
44	896	20.9	1507	1	SIMA_DROME	Q24167 drosophila
45	835	19.5	353	2	Q7PR97	Q7pr97 anopheles g

ALIGNMENTS

RESULT 1

HIFA_HUMAN

ID HIFA_HUMAN STANDARD; PRT; 826 AA.
AC Q16665; Q96PT9; Q9UPB1;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (HIF1 alpha) (ARNT
DE interacting protein) (Member of PAS protein 1) (MOP1).
GN Name=HIF1A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 166-170; 259-289 AND 771-781.
RX MEDLINE=95296340; PubMed=7539918;
RA Wang G.L., Jiang B.-H., Rue E.A., Semenza G.L.;
RT "Hypoxia-inducible factor 1 is a basic-helix-loop-helix-PAS
RT heterodimer regulated by cellular O2 tension";
RL Proc. Natl. Acad. Sci. U.S.A. 92:5510-5514(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Hepatoma;
RX MEDLINE=97236817; PubMed=9079689; DOI=10.1074/jbc.272.13.8581;
RA Hogenesch J.B., Chan W.K., Jackiw V.H., Brown R.C., Gu Y.-Z.,
RA Pray-Grant M., Perdew G.H., Bradfield C.A.;
RT "Characterization of a subset of the basic-helix-loop-helix-PAS
RT superfamily that interacts with components of the dioxin signaling
RT pathway";
RL J. Biol. Chem. 272:8581-8593(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=99000835; PubMed=9782081; DOI=10.1006/geno.1998.5416;

RA Iyer N.V., Leung S.W., Semenza G.L.;
 RT "The human hypoxia-inducible factor 1alpha gene: HIF1A structure and
 RT evolutionary conservation.";
 RL Genomics 52:159-165(1998).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Rupert J.L., Hochachka P.W.;
 RT "HIF1a sequence in the Quechua, a high altitude population.";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Glial tumor;
 RA Sun B., Zhao H.R., Yu R.T., Ni M.S.H.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Liver;
 RA Tanaka S., Sugimachi K.;
 RT "Hypoxia-inducible factor-1 alpha variant isolated from human liver
 RT tissue.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Choriocarcinoma, and Placenta;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP TRANSACTIVATION DOMAINS NTAD AND CTAD.
 RX MEDLINE=97382249; PubMed=9235919; DOI=10.1074/jbc.272.31.19253;
 RA Jiang B.H., Zheng J.Z., Leung S.W., Roe R., Semenza G.L.;
 RT "Transactivation and inhibitory domains of hypoxia-inducible factor
 RT 1alpha. Modulation of transcriptional activity by oxygen tension.";
 RL J. Biol. Chem. 272:19253-19260(1997).
 RN [9]
 RP SUBCELLULAR LOCATION, AND MUTAGENESIS OF LYS-719.
 RX MEDLINE=99043864; PubMed=9822602; DOI=10.1093/emboj/17.22.6573;
 RA Kallio P.J., Okamoto K., O'Brien S., Carrero P., Makino Y., Tanaka H.,
 RA Poellinger L.;
 RT "Signal transduction in hypoxic cells: inducible nuclear translocation
 RT and recruitment of the CBP/p300 coactivator by the hypoxia-inducible
 RT factor-1alpha.";
 RL EMBO J. 17:6573-6586(1998).
 RN [10]
 RP OXYGEN-DEPENDENT DEGRADATION DOMAIN.

us-09-922-958-4.rup

RX MEDLINE=98318598; PubMed=9653127; DOI=10.1073/pnas.95.14.7987;
RA Huang L.E., Gu J., Schau M., Bunn H.F.;
RT "Regulation of hypoxia-inducible factor 1alpha is mediated by an O2-
RT dependent degradation domain via the ubiquitin-proteasome pathway.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:7987-7992(1998).
RN [11]
RP TRANSACTIVATION DOMAINS NTAD AND CTAD, INTERACTION WITH APEX, AND
RP MUTAGENESIS OF CYS-800.
RX MEDLINE=99219869; PubMed=10202154; DOI=10.1093/emboj/18.7.1905;
RA Ema M., Hirota K., Mimura J., Abe H., Yodoi J., Sogawa K.,
RA Poellinger L., Fujii-Kuriyama Y.;
RT "Molecular mechanisms of transcription activation by HLF and HIF1alpha
RT in response to hypoxia: their stabilization and redox signal-induced
RT interaction with CBP/p300.";
RL EMBO J. 18:1905-1914(1999).
RN [12]
RP INTERACTION WITH NCOA1; NCOA2 AND APEX.
RX MEDLINE=20063199; PubMed=10594042;
RA Carrero P., Okamoto K., Coumaille P., O'Brien S., Tanaka H.,
RA Poellinger L.;
RT "Redox-regulated recruitment of the transcriptional coactivators CREB-
RT binding protein and SRC-1 to hypoxia-inducible factor 1alpha.";
RL Mol. Cell. Biol. 20:402-415(2000).
RN [13]
RP MUTAGENESIS OF SER-551 AND THR-552.
RX MEDLINE=20243767; PubMed=10758161; DOI=10.1073/pnas.080072497;
RA Sutter C.H., Laughner E., Semenza G.L.;
RT "Hypoxia-inducible factor 1alpha protein expression is controlled by
RT oxygen-regulated ubiquitination that is disrupted by deletions and
RT missense mutations.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4748-4753(2000).
RN [14]
RP UBIQUITINATION.
RX MEDLINE=21214630; PubMed=11292861; DOI=10.1126/science.1059796;
RA Jaakkola P., Mole D.R., Tian Y.-M., Wilson M.I., Gielbert J.,
RA Gaskell S.J., von Kriegsheim A., Hebestreit H.F., Mukherji M.,
RA Schofield C.J., Maxwell P.H., Pugh C.W., Ratcliffe P.J.;
RT "Targeting of HIF-alpha to the von Hippel-Lindau ubiquitylation
RT complex by O2-regulated prolyl hydroxylation.";
RL Science 292:468-472(2001).
RN [15]
RP S-NITROSYLATION.
RX MEDLINE=22448624; PubMed=12560087; DOI=10.1016/S0014-5793(02)03887-5;
RA Sumbayev V.V., Budde A., Zhou J., Bruene B.;
RT "HIF-1 alpha protein as a target for S-nitrosation.";
RL FEBS Lett. 535:106-112(2003).
RN [16]
RP ACETYLTATION OF LYS-532.
RX MEDLINE=22351901; PubMed=12464182; DOI=10.1016/S0092-8674(02)01085-1;
RA Jeong J.-W., Bae M.-K., Ahn M.-Y., Kim S.-H., Sohn T.-K., Bae M.-H.,
RA Yoo M.-A., Song E.-J., Lee K.-J., Kim K.-W.;
RT "Regulation and destabilization of HIF-1alpha by ARD1-mediated
RT acetylation.";
RL Cell 111:709-720(2002).
RN [17]
RP HYDROXYLTATION OF ASN-803.
RX MEDLINE=22074910; PubMed=12080085; DOI=10.1101/gad.991402;
RA Lando D., Peet D.J., Gorman J.J., Whelan D.A., Whitelaw M.L.,
RA Bruick R.K.;
RT "FIH-1 is an asparaginyl hydroxylase enzyme that regulates the
RT transcriptional activity of hypoxia-inducible factor.";
RL Genes Dev. 16:1466-1471(2002).
RN [18]

us-09-922-958-4.rup

RP HYDROXYLATION OF PRO-402 AND PRO-564.
RX MEDLINE=21558830; PubMed=11598268; DOI=10.1126/science.1066373;
RA Bruick R.K., McKnight S.L.;
RT "A conserved family of prolyl-4-hydroxylases that modify HIF.";
RL Science 294:1337-1340(2001).
RN [19]
RP REVIEW.
RX MEDLINE=20407247; PubMed=10950862;
RA Semenza G.L.;
RT "HIF-1 and human disease: one highly involved factor.";
RL Genes Dev. 14:1983-1991(2000).
RN [20]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=20539371; PubMed=11089639;
RA Michel G., Minet E., Ernest I., Roland I., Durant F., Remacle J.,
RA Michiels C.;
RT "A model for the complex between the hypoxia-inducible factor-1 (HIF-
RT 1) and its consensus DNA sequence.";
RL J. Biomol. Struct. Dyn. 18:169-179(2000).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF 775-826 IN COMPLEX WITH
RP HIF1AN.
RX MEDLINE=22412289; PubMed=12446723; DOI=10.1074/jbc.C200644200;
RA Elkins J.M., Hewitson K.S., McNeill L.A., Seibel J.F.,
RA Schlemminger I., Pugh C.W., Ratcliffe P.J., Schofield C.J.;
RT "Structure of factor-inhibiting hypoxia-inducible factor (HIF) reveals
RT mechanism of oxidative modification of HIF-1 alpha.";
RL J. Biol. Chem. 278:1802-1806(2003).
RN [22]
RP STRUCTURE BY NMR OF 786-826 IN COMPLEX WITH 302-418 OF EP300.
RX MEDLINE=21957254; PubMed=11959990; DOI=10.1073/pnas.082117899;
RA Freedman S.J., Sun Z.-Y.J., Poy F., Kung A.L., Livingston D.M.,
RA Wagner G., Eck M.J.;
RT "Structural basis for recruitment of CBP/p300 by hypoxia-inducible
RT factor-1 alpha.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:5367-5372(2002).
RN [23]
RP STRUCTURE BY NMR OF 776-826 IN COMPLEX WITH 345-439 OF CREBBP.
RX MEDLINE=21957241; PubMed=11959977; DOI=10.1073/pnas.082121399;
RA Dames S.A., Martinez-Yamout M., De Guzman R.N., Dyson H.J.,
RA Wright P.E.;
RT "Structural basis for Hif-1 alpha /CBP recognition in the cellular

Query Match 100.0%; Score 4287; DB 1; Length 826;
Best Local Similarity 100.0%; Pred. No. 7.5e-208;
Matches 826; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEGAGGANDKKKISSERRKEKSRDAARSRRSKESEVFYELAHQLPLPHNVSSHLDKASVM	60
Db	1	MEGAGGANDKKKISSERRKEKSRDAARSRRSKESEVFYELAHQLPLPHNVSSHLDKASVM	60
QY	61	RLTISYLRVRKLLDAGDLIEDDMKAQMNCFYLKALDGFVMVLTDGDMIYISDNVNKYM	120
Db	61	RLTISYLRVRKLLDAGDLIEDDMKAQMNCFYLKALDGFVMVLTDGDMIYISDNVNKYM	120
QY	121	GLTQFELTGHSVFDFTHPCDHEEMREMLTHRNLVKKGKEQNTQRSFFLRMKCTLTSGR	180
Db	121	GLTQFELTGHSVFDFTHPCDHEEMREMLTHRNLVKKGKEQNTQRSFFLRMKCTLTSGR	180
QY	181	TMNIKSATWKVLHCTGHIHVYDTNSNQPCGYKKPPMTCLVLICEPIPHPSNIEIPLDSK	240
Db	181	TMNIKSATWKVLHCTGHIHVYDTNSNQPCGYKKPPMTCLVLICEPIPHPSNIEIPLDSK	240

us-09-922-958-4.rup

Qy	241	TFLSRHSLDMKFSYCDERITELMGYEPEELLGRSIEYYHALDSDHCLKTHHDMFTKGQV	300
Db	241	TFLSRHSLDMKFSYCDERITELMGYEPEELLGRSIEYYHALDSDHCLKTHHDMFTKGQV	300
Qy	301	TTGQYRMLAKRGGYVWVETQATVIYNTKNSQPQCIVCVNYVSGIIQHDLIFSLQQTECV	360
Db	301	TTGQYRMLAKRGGYVWVETQATVIYNTKNSQPQCIVCVNYVSGIIQHDLIFSLQQTECV	360
Qy	361	LKPVESSDMKMTQLFTKVESEDTSSEFDKLLKKEPDALTLLAPAAGDTIISLDFGSNDTET	420
Db	361	LKPVESSDMKMTQLFTKVESEDTSSEFDKLLKKEPDALTLLAPAAGDTIISLDFGSNDTET	420
Qy	421	DDQQLLEEVPLYNDVMLPSPNEKLQINLAMSPLETPKPLRSSADPALNQEVALKLEP	480
Db	421	DDQQLLEEVPLYNDVMLPSPNEKLQINLAMSPLETPKPLRSSADPALNQEVALKLEP	480
Qy	481	NPESLELSFTMPQIQDQTPSPSDGSTRQSSPEPNPSEYCFYVDSMDVNEFKLELVEKLF	540
Db	481	NPESLELSFTMPQIQDQTPSPSDGSTRQSSPEPNPSEYCFYVDSMDVNEFKLELVEKLF	540
Qy	541	AEDTEAKNPFSTQDQDLDLEMLAPYIPMDDDFQLRSFDQLSPLESSSASPESASPSTVT	600
Db	541	AEDTEAKNPFSTQDQDLDLEMLAPYIPMDDDFQLRSFDQLSPLESSSASPESASPSTVT	600
Qy	601	VFQQTQIQEPTANATTTTATTDDELKTVTKDRMEDIKILIASPSPTHIHKETTSATSSPYR	660
Db	601	VFQQTQIQEPTANATTTTATTDDELKTVTKDRMEDIKILIASPSPTHIHKETTSATSSPYR	660
Qy	661	DTQSRTASPNRAGKGVIEQTEKSHPRSPNVLSVALSQRTTVPEEELNPKILALQNAQRKR	720
Db	661	DTQSRTASPNRAGKGVIEQTEKSHPRSPNVLSVALSQRTTVPEEELNPKILALQNAQRKR	720
Qy	721	KMEHDGSLFQAVGIGTLLQQPDDHAATTSLSWKRKVGCKSSEQNGMEQKTIILIPSDLAC	780
Db	721	KMEHDGSLFQAVGIGTLLQQPDDHAATTSLSWKRKVGCKSSEQNGMEQKTIILIPSDLAC	780
Qy	781	RLLGQSMDESGLPQLTSYDCEVNAPIQGSRNLLQGEELLRALDQVN	826
Db	781	RLLGQSMDESGLPQLTSYDCEVNAPIQGSRNLLQGEELLRALDQVN	826

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 27, 2005, 07:32:56 ; Search time 14.1136 Seconds
(without alignments)
1479.779 Million cell updates/sec

Title: US-09-922-958-5
Perfect score: 275
Sequence: 1 KLELVEKLFAEDTEAKNPFs.....IPMDDDFQLRSFDQLSPLES 54

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	275	100.0	54	7	AAO23490	Aao23490 Murine HI
2	275	100.0	116	3	AAy94632	Aay94632 HIF-1alph
3	275	100.0	288	3	AAy94633	Aay94633 HIF-1alph
4	275	100.0	301	3	AAy94634	Aay94634 HIF-1alph
5	275	100.0	311	3	AAy94631	Aay94631 HIF-1alph
6	275	100.0	409	8	ADO39389	Ado39389 Chimeric
7	275	100.0	444	4	AAB68415	Aab68415 Amino aci
8	275	100.0	466	8	ADO39390	Ado39390 Chimeric
9	275	100.0	538	8	ADO39387	Ado39387 Chimeric

10	275	100.0	542	5	ABP41474	Abp41474	Human ova
11	275	100.0	595	8	ADO39388	Ado39388	Chimeric
12	275	100.0	613	3	AAy94630	Aay94630	HIF-lalph
13	275	100.0	613	5	AAU77614	Aau77614	Human hyp
14	275	100.0	632	8	ADO39391	Ado39391	Chimeric
15	275	100.0	652	3	AAy94629	Aay94629	HIF-lalph
16	275	100.0	735	6	ABR82375	Abr82375	Hypoxia-i
17	275	100.0	735	8	ADN75066	Adn75066	Human hyp
18	275	100.0	756	3	AAy94635	Aay94635	HIF-lalph
19	275	100.0	805	2	AAW06558	Aaw06558	Hypoxia i
20	275	100.0	810	5	ABB57270	Abb57270	Mouse isc
21	275	100.0	813	3	AAy94636	Aay94636	HIF-lalph
22	275	100.0	826	2	AAW06557	Aaw06557	Human hyp
23	275	100.0	826	2	AAW80418	Aaw80418	Amino aci
24	275	100.0	826	2	AAy06289	Aay06289	Human tra
25	275	100.0	826	3	AAy69407	Aay69407	A wild ty
26	275	100.0	826	3	AAy94640	Aay94640	Human hyp
27	275	100.0	826	4	AAB76854	Aab76854	Human lun
28	275	100.0	826	5	AAU85509	Aau85509	Clone #19
29	275	100.0	826	5	AAU77602	Aau77602	Human hyp
30	275	100.0	826	5	AAU77613	Aau77613	Human hyp
31	275	100.0	826	5	AAE24212	Aae24212	Human HIF
32	275	100.0	826	5	AAU69409	Aau69409	Lung smal
33	275	100.0	826	6	AAE30021	Aae30021	Human hyp
34	275	100.0	826	6	AAE30168	Aae30168	Human HIF
35	275	100.0	826	6	ABP55438	Abp55438	Human hyp
36	275	100.0	826	6	ABU69481	Abu69481	Human lun
37	275	100.0	826	6	ABR40380	Abr40380	Human HIF
38	275	100.0	826	6	ABU89720	Abu89720	Protein d
39	275	100.0	826	6	AAG79969	Aag79969	Human Hif
40	275	100.0	826	6	ABU66383	Abu66383	Lung canc
41	275	100.0	826	6	ADA18531	Adal8531	Human hyp
42	275	100.0	826	6	ABR82374	Abr82374	Hypoxia-i
43	275	100.0	826	7	ADD18956	Add18956	Human dis
44	275	100.0	826	7	ADD44857	Add44857	Human Pro
45	275	100.0	826	7	ADH45849	Adh45849	Human lun

ALIGNMENTS

RESULT 1

AAO23490

ID AAO23490 standard; peptide; 54 AA.

XX

AC AAO23490;

XX

DT 12-FEB-2004 (first entry)

XX

DE Murine HIF-lalpha protein N-TAD region fragment (residues 531-584).

XX

KW HIF-lalpha; hypoxia-inducible factor -lalpha; vasotropic; antidiabetic;

KW ophthalmological; antiinflammatory; cardiant; antirheumatic; mouse;

KW antiarthritic; cerebroprotective; angiogenesis stimulator; gene therapy;

KW N-TAD.

XX

OS Mus sp.

XX
 PN WO2003074560-A2.
 XX
 PD 12-SEP-2003.
 XX
 PF 05-MAR-2003; 2003WO-SE000372.
 XX
 PR 05-MAR-2002; 2002US-0361333P.
 PR 27-NOV-2002; 2002US-0429307P.
 XX
 PA (ANGI-) ANGIOGENETICS SWEDEN AB.
 XX
 PI Pereira T, Poellinger L, Hellstroem M;
 XX
 DR WPI; 2003-712876/67.
 XX
 PT New hypoxia-inducible factor (HIF)-1alpha protein, useful for increasing
 PT angiogenesis, or treating a condition associated with HIF-1alpha
 PT underexpression in a cell, a group of cells, or an organism, e.g.
 PT ischemia or inflammation.
 XX
 PS Example 4; Fig 4; 96pp; English.
 XX
 CC The invention relates to a hypoxia-inducible factor (HIF)-1alpha protein
 CC that has (a) an altered transactivation capacity and improved stability
 CC at normoxia. The HIF-1alpha protein, polynucleotide, vector, and
 CC pharmaceutical composition are useful for increasing angiogenesis,
 CC interfering with a normal response to reoxygenation following hypoxia, or
 CC treating a condition associated with HIF-1alpha underexpression in a
 CC cell, a group of cells, or an organism, e.g. ischaemia, diabetic
 CC retinopathy, inflammation, coronary heart disease, rheumatoid arthritis,
 CC stroke. The proteins and pharmaceutical compositions are also useful for
 CC mimicking the hypoxic response or artificially inducing a hypoxic
 CC response in a cell, group of cells, or organism, inducing vascular
 CC formation or vascular development in a cell or a group of cells,
 CC increasing angiogenetic activity in a cell, or influencing erythropoietin
 CC production, metabolism, or an inflammatory response in a cell, a group of
 CC cells, or an organism. The present sequence represents a N-TAD region of
 CC a murine HIF-1 alpha protein
 XX
 SQ Sequence 54 AA;

Query Match 100.0%; Score 275; DB 7; Length 54;
 Best Local Similarity 100.0%; Pred. No. 1.1e-28;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLELVEKLFAEDTEAKNPFSTQDTLDLEMLAPYIPMDDDFQLRSFDQLSPLES 54
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 1 KLELVEKLFAEDTEAKNPFSTQDTLDLEMLAPYIPMDDDFQLRSFDQLSPLES 54

RESULT 2
 AAY94632
 ID AAY94632 standard; protein; 116 AA.
 XX
 AC AAY94632;
 XX

DT 15-AUG-2000 (first entry)
 XX
 DE HIF-1alpha variant protein sequence HIF-1alpha/526-641.
 XX
 KW Hypoxia-inducible factor 1alpha; HIF-1alpha; PAS-B; N-TAD; C-TAD; ~
 KW regulation; angiogenesis; erythropoiesis; glycolysis; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200029437-A1.
 XX
 PD 25-MAY-2000.
 XX
 PF 11-NOV-1999; 99WO-SE002053.
 XX
 PR 13-NOV-1998; 98SE-00003891.
 XX
 PA (PHAA) PHARMACIA & UPJOHN AB.
 XX
 PI Berkenstam A, Poellinger L;
 XX
 DR WPI; 2000-399715/34.
 XX
 PT Human hypoxia-inducible factor alpha variants for identifying compounds
 PT that modulate its functional domain and regulate genes involved in
 PT angiogenesis, erythropoiesis.
 XX
 PS Claim 13; Page 76-77; 87pp; English.
 XX
 CC This sequence represents a fragment of the hypoxia-inducible factor (HIF)
 CC -1alpha amino acid sequence. The mechanism of action of HIF-1alpha is a
 CC multi-step process which includes hypoxia-dependent nuclear import and
 CC activation of the transactivation domain. The HIF-1alpha consists of a
 CC number of functional domains including a PAS-B (Per, Arnt, Sim) domain
 CC located in human HIF-1alpha between amino acids 173 and 390, a C-terminal
 CC nuclear localization sequence located at amino acids 718-584, a
 CC transactivator domain (N-TAD) located between amino acids 531 and 584,
 CC and a second transactivator domain (C-TAD) located between 813 and 826.
 CC The invention relates to isolated variants of HIF-1alpha, such as that
 CC represented by the present sequence. The variants are useful for
 CC identifying compounds capable of modulating the function of a functional
 CC domain of human HIF-1alpha. The method comprises contacting a candidate
 CC compound with a cell expressing a HIF-1alpha variant conjugated to a
 CC molecular probe. The localization of the probe can be detected in the
 CC cell. The Aequorea victoria green fluorescent protein can be used as the
 CC molecular probe. The compounds are useful for the regulation of HIF-
 CC 1alpha target genes, such as those involved in the regulation of
 CC angiogenesis, erythropoiesis an glycolysis
 XX
 SQ Sequence 116 AA;

Query Match 100.0%; Score 275; DB 3; Length 116;
 Best Local Similarity 100.0%; Pred. No. 2.8e-28;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLELVEKLFAEDTEAKNPFSTQDLDLEMLAPYIPMDDDFQLRSFDQLSPLES 54
 |||

Db

7 KLELVEKLFAEDTEAKNPFSTQDTDLLEMLAPYIPMDDDFQLRSFDQLSPLES 60

us-09-922-958-5.rapb

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 27, 2005, 07:53:38 ; Search time 13.3159 Seconds
(without alignments)
1577.480 Million cell updates/sec

Title: US-09-922-958-5
Perfect score: 275
Sequence: 1 KLELVEKLFAEDTEAKNPFS.....IPMDDDFQLRSFDQLSPLES 54

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	275	100.0	54	9	US-09-922-958-5	Sequence 5, Appli

				us-09-922-958-5.rapb		
2	275	100.0	409	15	US-10-425-833-8	Sequence 8, Appli
3	275	100.0	466	15	US-10-425-833-9	Sequence 9, Appli
4	275	100.0	538	15	US-10-425-833-6	Sequence 6, Appli
5	275	100.0	542	15	US-10-264-049-2606	Sequence 2606, Ap
6	275	100.0	595	15	US-10-425-833-7	Sequence 7, Appli
7	275	100.0	735	16	US-10-032-361-2	Sequence 2, Appli
8	275	100.0	826	9	US-09-922-958-4	Sequence 4, Appli
9	275	100.0	826	9	US-09-833-790-235	Sequence 235, App
10	275	100.0	826	9	US-09-736-457-330	Sequence 330, App
11	275	100.0	826	9	US-09-902-941-330	Sequence 330, App
12	275	100.0	826	9	US-09-849-626-330	Sequence 330, App
13	275	100.0	826	10	US-09-967-388-4	Sequence 4, Appli
14	275	100.0	826	10	US-09-476-300-330	Sequence 330, App
15	275	100.0	826	13	US-10-028-158-23	Sequence 23, Appl
16	275	100.0	826	13	US-10-101-812-10	Sequence 10, Appl
17	275	100.0	826	14	US-10-101-662A-9	Sequence 9, Appli
18	275	100.0	826	14	US-10-017-754-330	Sequence 330, App
19	275	100.0	826	14	US-10-115-987B-14	Sequence 14, Appl
20	275	100.0	826	14	US-10-287-670-9	Sequence 9, Appli
21	275	100.0	826	14	US-10-113-872-330	Sequence 330, App
22	275	100.0	826	14	US-10-423-419-2	Sequence 2, Appli
23	275	100.0	826	15	US-10-283-017-330	Sequence 330, App
24	275	100.0	826	16	US-10-032-361-1	Sequence 1, Appli
25	275	100.0	826	16	US-10-859-935-10	Sequence 10, Appl
26	275	100.0	826	16	US-10-859-935-23	Sequence 23, Appl
27	275	100.0	826	17	US-10-901-583-18	Sequence 18, Appl
28	275	100.0	826	18	US-10-472-595A-35	Sequence 35, Appl
29	275	100.0	826	20	US-11-043-493-23	Sequence 23, Appl
30	275	100.0	827	10	US-09-919-039-149	Sequence 149, App
31	275	100.0	827	14	US-10-247-671-137	Sequence 137, App
32	275	100.0	836	18	US-10-988-486-6	Sequence 6, Appli
33	270	98.2	823	14	US-10-205-342-13	Sequence 13, Appl
34	270	98.2	826	14	US-10-101-816-5	Sequence 5, Appli
35	270	98.2	826	16	US-10-854-483-5	Sequence 5, Appli
36	267	97.1	826	14	US-10-101-816-2	Sequence 2, Appli
37	267	97.1	826	16	US-10-854-483-2	Sequence 2, Appli
38	264	96.0	632	15	US-10-425-833-10	Sequence 10, Appl
39	262	95.3	826	14	US-10-101-816-6	Sequence 6, Appli
40	262	95.3	826	14	US-10-101-816-7	Sequence 7, Appli
41	262	95.3	826	16	US-10-854-483-6	Sequence 6, Appli
42	262	95.3	826	16	US-10-854-483-7	Sequence 7, Appli
43	180	65.5	34	17	US-10-901-583-9	Sequence 9, Appli
44	180	65.5	34	18	US-10-472-595A-16	Sequence 16, Appl
45	180	65.5	34	18	US-10-472-595A-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-09-922-958-5
; Sequence 5, Application US/09922958
; Patent No. US20020048794A1
; GENERAL INFORMATION:
; APPLICANT: POELLINGER, Lorenz
; APPLICANT: PEREIRA, Teresa
; APPLICANT: RUAS, Jorge
; TITLE OF INVENTION: MECHANISM OF CONDITIONAL REGULATION OF THE HYPOXIA-INDUCIBLE
FACTOR-1 BY
; TITLE OF INVENTION: THE VON HIPPEL-LINDAU TUMOR SUPPRESSOR PROTEIN
; FILE REFERENCE: 3743/49008
; CURRENT APPLICATION NUMBER: US/09/922,958
; CURRENT FILING DATE: 2001-08-07

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; PRIOR APPLICATION NUMBER: US 60/223,480
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 54
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-922-958-5

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Query Match 100.0%; Score 275; DB 9; Length 54;
Best Local Similarity 100.0%; Pred. No. 4e-27;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLELVEKLF AEDTEAKNPFSTQD TLDLEMLAPYIPMDDDFQLRSFDQLSPLES 54
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 db 1 KLELVEKLF AEDTEAKNPFSTQD TLDLEMLAPYIPMDDDFQLRSFDQLSPLES 54

RESULT 2

US-10-425-833-8

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00 10 125 000 0
: Sequence 8, Application US/10425833

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: Publication No. US20040018606A1

; GENERAL INFORMATION:

APPLICANT: Boh1, Delphine

; APPLICANT: Heard, Jean Michael

; TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HIF1-alpha

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; TITLE OF INVENTION: chimeric transactivator
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; FILE REFERENCE: 235748US0

; CURRENT APPLICATION NUMBER: US/10/425,833

; CURRENT FILING DATE: 2003-04-30

; PRIOR APPLICATION NUMBER: US 60/376,269

; PRIOR FILING DATE: 2002-04-30
NUMBER OF SEQ. TO NOS: 10

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; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Retention viewer;
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; SOFTWARE: PatentIn version 3.1
; GEO ID: NO. 8

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; SEQ ID NO 8
; LENGTH: 400
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; LENGTH: 4
; TYPE: PBT

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: TYPE: PRI
: ORGANISM: ARTIFICIAL SEQUENCE

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: ORGANISM: ARTIFICIAL SEQUENCE

FEATURE:

: OTHER INFORMATION: SYNTHETIC PEPTIDE

US-10-425-833-8

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Best Local Similarity 100.0%; Pred. No. 4.4e-26;

Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 211 KLELVEKLFAEDTEAKNPFSTQDLDLEMLAPYIPMDDDFQLRSFDQLSPLES 264

RESULT 3

US-10-425-833-9

; Sequence 9, Application US/10425833

; GENERAL INFORMATION:

; APPLICANT: Boh1, Delphine

; APPLICANT: Heard, Jean Michael

; TITLE OF INVENTION: Control of protein systemic delivery of hypoxia using a tet-HIF1- α

us-09-922-958-5.rapb

; FILE REFERENCE: 235748US0
; CURRENT APPLICATION NUMBER: US/10/425,833
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/376,269
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 466
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-425-833-9

Query Match 100.0%; Score 275; DB 15; Length 466;
Best Local Similarity 100.0%; Pred. No. 5.1e-26;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 211 KLELVEKLFAEDTEAKNPFSTQDLDLEMLAPYIPMDDDFQLRSFDQLSPLES 264

GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
1628.284 Million cell updates/sec

Title: US-09-922-958-5
Perfect score: 275
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 283416

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	270	98.2	813	2	JC5809		hypoxia-inducible
4	263	95.6	811	2	JC7619		hypoxia-inducible
5	112.5	40.9	667	2	JC7771		hypoxia inducible
6	69	25.1	241	2	I64154		conserved hypothet
7	68	24.7	243	2	AB0477		probable peroxired
8	67	24.4	245	2	G81140		peroxiredoxin 2 fa
9	67	24.4	247	2	D82051		peroxiredoxin fami
10	64.5	23.5	1505	2	JC4851		hypoxia-inducible
11	64	23.3	440	2	S74197		ATP-dependent 26S
12	62.5	22.7	294	2	E81420		probable flagellar
13	62.5	22.7	3587	2	T31075		tyrocidine synthet

14	62	22.5	139	2	D90303	hypothetical prote
15	62	22.5	440	2	A44468	26S proteasome reg
16	62	22.5	1169	2	F95000	transcription-repa
17	62	22.5	1169	2	F97872	transcriptiorepair
18	61.5	22.4	751	2	AG1329	penicillin-binding
19	61.5	22.4	752	2	AG1700	penicillin-binding
20	61.5	22.4	1827	1	UUHU	sucrose alpha-gluc
21	60.5	22.0	596	2	F84589	probable protein k
22	60.5	22.0	822	2	T33163	hypothetical prote
23	60.5	22.0	5369	2	T44807	mycosubtilin synth
24	60	21.8	310	1	S37695	calcium-binding pr
25	59.5	21.6	429	2	T04667	cyclin 2b - Arabid
26	58	21.1	380	1	WZZMP	dihydrodipicolinat
27	58	21.1	557	2	T41631	hypothetical prote
28	57	20.7	579	2	D84137	methyl-accepting c
29	56.5	20.5	760	2	E84953	penicillin-binding c
30	56.5	20.5	936	2	E87115	pyruvate dehydroge
31	56	20.4	156	1	WZBE25	gene 25 protein -
32	56	20.4	326	2	H83105	conserved hypothet
33	56	20.4	1785	2	T22595	hypothetical prote
34	55.5	20.2	303	2	D95011	hypothetical prote
35	55.5	20.2	320	2	G97882	hypothetical prote
36	55.5	20.2	548	2	S50557	hypothetical prote
37	55.5	20.2	759	2	I49007	hormone-sensitive
38	55	20.0	162	2	F90549	conserved hypothet
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40	55	20.0	770	2	S37963	mitochondrial inte
41	55	20.0	1112	2	T40382	dna repair protein
42	55	20.0	1113	2	S30301	excision repair pr
43	55	20.0	1650	2	T18444	hypothetical prote
44	55	20.0	2607	2	T31678	bacitracin synthet
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ALIGNMENTS

RESULT 1

JC4837

hypoxia-inducible factor 1 alpha - mouse

C;Species: Mus musculus (house mouse)

C;Date: 15-Aug-1996 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004

C;Accession: JC4837

R;Wenger, R.H.; Rolfs, A.; Marti, H.H.; Guenet, J.L.; Gassmann, M.

Biochem. Biophys. Res. Commun. 223, 54-59, 1996

A;Title: Nucleotide sequence, chromosomal assignment and mRNA expression of mouse hypoxia-inducible factor-1 alpha.

A;Reference number: JC4837; MUID:96254028; PMID:8660378

A;Accession: JC4837

A;Molecule type: mRNA

A;Residues: 1-810 <WEN>

A;Cross-references: UNIPROT:Q61221; EMBL:X95580; NID:gl430864; PIDN:CAA64833.1; PID:g4379202

C;Comment: This factor is involved in the oxygen-regulated transcription of several genes including erythropoietin.

C;Genetics:

A;Gene: Hif1alpha

A;Map position: 12
C;Keywords: transcription factor
F;5-58/Region: helix-loop-helix #status predicted

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Best Local Similarity 100.0%; Pred. No. 2.2e-25;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLELVEKLFAEDTEAKNPFSTQDLDLEMLAPYIPMDDDFQLRSFDQLSPLES 54
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RESULT 2

I38972

hypoxia-inducible factor 1 alpha - human

N;Alternate names: ARNT interacting protein

C;Species: Homo sapiens (man)

C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004

C;Accession: I38972; G01875

R;Wang, G.L.; Jiang, B.H.; Rue, E.A.; Semenza, G.L.

Proc. Natl. Acad. Sci. U.S.A. 92, 5510-5514, 1995

A;Title: Hypoxia-inducible factor 1 is a basic-helix-loop-helix-PAS heterodimer regulated by cellular O2 tension.

A;Reference number: I38972; MUID:95296340; PMID:7539918

A;Accession: I38972

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-826 <RES>

A;Cross-references: UNIPROT:Q16665; EMBL:U22431; NID:g881345; PIDN:AAC50152.1; PID:g881346

A;Note: parts of this sequence were confirmed by peptide sequencing

R;Hogenesch, J.B.; Chan, W.K.; Carver, L.A.; Bradfield, C.A.

submitted to the EMBL Data Library, June 1995

A;Reference number: H00692

A;Accession: G01875

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-826 <HOG>

A;Cross-references: EMBL:U29165; NID:g1144012; PIDN:AAC51210.1; PID:g1144013

C;Genetics:

A;Gene: GDB:HIF1A

A;Cross-references: GDB:512229

A;Map position: 14q21-14q24

C;Keywords: heterodimer

Query Match 100.0%; Score 275; DB 2; Length 826;
Best Local Similarity 100.0%; Pred. No. 2.3e-25;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLELVEKLFAEDTEAKNPFSTQDLDLEMLAPYIPMDDDFQLRSFDQLSPLES 54
|||||
Db 532 KLELVEKLFAEDTEAKNPFSTQDLDLEMLAPYIPMDDDFQLRSFDQLSPLES 585

RESULT 3

JC5809

hypoxia-inducible factor 1 alpha - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 26-Aug-1999
 C;Accession: JC5809
 R;Ladoux, A.; Frelin, C.
 Biochem. Biophys. Res. Commun. 240, 552-556, 1997
 A;Title: Cardiac expressions of HIF-1 alpha and HLF/EPAS, two basic loop
 helix/PAS domain transcription factors involved in adaptative responses to
 hypoxic stresses.
 A;Reference number: JC5809; MUID:98063274; PMID:9398602
 A;Accession: JC5809
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-813 <LAD>
 C;Comment: This protein associates to the aryl hydrocarbon receptor nuclear
 translocator, binds to specific hypoxia responsive elements and activates the
 transcription of hypoxia sensitive genes such as erythropoietin, vascular
 endothelial growth factor, the GLUT1 glucose transporter, enzymes of glycolysis
 and the inducible form of nitric oxyde synthase.
 F;6-144/Region: basic helix-loop-helix #status predicted

Query Match 98.2%; Score 270; DB 2; Length 813;
 Best Local Similarity 98.1%; Pred. No. 9e-25;
 Matches 53; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 KLELVEKLFAEDTEAKNPFSTQDTDLDEMLAPYIPMDDDFQLRSFDQLSPLES 54
          |||
Db      519 KLELVEKLFAEDTEAKNPFSAQDTDLDEMLAPYIPMDDDFQLRSFDQLSPLES 572

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us-09-922-958-5.rup

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 27, 2005, 07:33:41 ; Search time 13.9295 Seconds
(without alignments)
1985.153 Million cell updates/sec

Title: US-09-922-958-5
Perfect score: 275
Sequence: 1 KLELVEKLFAEDTEAKNPFS.....IPMDDDFQLRSFDQLSPLES 54

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	275	100.0	786	2	Q6SLL1	Q6sll1 canis famil
2	275	100.0	819	2	Q7YSE5	Q7yse5 oryctolagus
3	275	100.0	821	2	Q64F54	Q64f54 spermophilu
4	275	100.0	826	1	HIFA_HUMAN	Q16665 homo sapien
5	275	100.0	836	1	HIFA_MOUSE	Q61221 mus musculu
6	272	98.9	823	1	HIFA_BOVIN	Q9xta5 bos taurus
7	272	98.9	823	2	Q6IV47	Q6iv47 bos mutus g
8	270	98.2	825	1	HIFA_RAT	Q35800 rattus norv
9	269	97.8	824	2	Q6H8T3	Q6h8t3 spalax juda
10	263	95.6	811	1	HIFA_CHICK	Q9yib9 gallus gall
11	234	85.1	802	2	Q6PI54	Q6pi54 xenopus lae
12	210	76.4	805	1	HIFA_XENLA	Q9i8a9 xenopus lae
13	196.5	71.5	777	2	Q6EHI4	Q6ehi4 brachydanio
14	187.5	68.2	774	2	Q6STN7	Q6stn7 ctenopharyn
15	159.5	58.0	766	1	HIFA_ONCMY	Q98sw2 oncorhynchu
16	146	53.1	862	2	Q6GP97	Q6gp97 xenopus lae
17	144	52.4	862	2	Q6GL61	Q6gl61 xenopus tro
18	143	52.0	859	2	Q6GQ12	Q6gq12 xenopus lae
19	141.5	51.5	874	1	PAS1_MOUSE	P97481 mus musculu
20	141.5	51.5	874	1	PAS1_RAT	Q9jhs1 rattus norv
21	141.5	51.5	874	2	Q6PEU2	Q6peu2 mus musculu

					us-09-922-958-5.rup	
22	139.5	50.7	870	1	PAS1_HUMAN	Q99814 homo sapien
23	135	49.1	164	2	Q6RYD0	Q6ryd0 ovis aries
24	135	49.1	870	2	Q9XTA4	Q9xta4 bos taurus
25	132	48.0	163	2	Q6RYD1	Q6ryd1 sus scrofa
26	129.5	47.1	867	2	Q9W7C6	Q9w7c6 gallus gall
27	129.5	47.1	870	2	Q9PTB3	Q9ptb3 coturnix co
28	122	44.4	835	2	Q696W2	Q696w2 ctenopharyn
29	118.5	43.1	873	2	Q8QGM4	Q8qgm4 fundulus he
30	112.5	40.9	632	2	Q8WXA1	Q8wxa1 homo sapien
31	112.5	40.9	648	2	Q9HAI2	Q9hai2 homo sapien
32	112.5	40.9	667	2	Q9Y2N7	Q9y2n7 homo sapien
33	112.5	40.9	669	2	Q66K72	Q66k72 homo sapien
34	107.5	39.1	630	2	Q9QX54	Q9qx54 mus musculu
35	107.5	39.1	662	2	Q9Z2I5	Q9z2i5 mus musculu
36	107	38.9	662	2	Q9JHS2	Q9jhs2 rattus norv
37	105.5	38.4	632	2	Q96K34	Q96k34 homo sapien
38	104	37.8	571	2	Q7T2E4	Q7t2e4 brachydanio
39	104	37.8	626	2	Q6EGR9	Q6egr9 brachydanio
40	103.5	37.6	643	2	Q6STN6	Q6stn6 ctenopharyn
41	77.5	28.2	235	2	Q8QGI5	Q8qgi5 fundulus he
42	69	25.1	241	1	Y572_HAEIN	P44758 haemophilus
43	69	25.1	253	2	Q75TM4	Q75tm4 actinobacil
44	68	24.7	243	2	Q66G63	Q66g63 yersinia ps
45	68	24.7	243	2	Q8ZA95	Q8za95 yersinia pe

ALIGNMENTS

RESULT 1

Q6SLL1

ID Q6SLL1 PRELIMINARY; PRT; 786 AA.
AC Q6SLL1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypoxia-inducible factor 1 alpha subunit (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Spee B., Penning L.C., Rothuizen J.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY455802; AAR19225.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR001321; HypoxindF1A.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 2.
DR PRINTS; PR01080; HYPOXIAIF1A.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50112; PAS; 2.

us-09-922-958-5.rup

FT NON_TER 1 1
FT NON_TER 786 786
SQ SEQUENCE 786 AA; 88015 MW; C37A27C25C343CDC CRC64;

Query Match 100.0%; Score 275; DB 2; Length 786;
Best Local Similarity 100.0%; Pred. No. 2.7e-24;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLELVEKLFAEDTEAKNPFSTQDSDLLEMLAPYIPMDDDFQLRSFDQLSPLES 54
|||
Db 512 KLELVEKLFAEDTEAKNPFSTQDSDLLEMLAPYIPMDDDFQLRSFDQLSPLES 565

RESULT 2

Q7YSE5

ID Q7YSE5 PRELIMINARY; PRT; 819 AA.
AC Q7YSE5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypoxia inducible factor 1 alpha subunit.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Clausen I., Kietz S., Fischer B.;
RL Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AY273790; AAP43517.1; -.
DR HSSP; Q16665; 1H2K.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS.
DR Pfam; PF00010; HLH; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 2.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00086; PAC; 1.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS50888; HLH; 1.
DR PROSITE; PS50112; PAS; 2.
SQ SEQUENCE 819 AA; 91284 MW; E11B4FBF7D4F6C7C CRC64;

Query Match 100.0%; Score 275; DB 2; Length 819;
Best Local Similarity 100.0%; Pred. No. 2.8e-24;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLELVEKLFAEDTEAKNPFSTQDSDLLEMLAPYIPMDDDFQLRSFDQLSPLES 54
|||
Db 532 KLELVEKLFAEDTEAKNPFSTQDSDLLEMLAPYIPMDDDFQLRSFDQLSPLES 585

us-09-922-958-4.ra1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 27, 2005, 07:43:11 ; Search time 56.3182 Seconds
(without alignments)
1094.853 Million cell updates/sec

Title: US-09-922-958-4
Perfect score: 4287
Sequence: 1 MEGAGGANDKKKISSERRKE.....QGSRNLLQGEELLRALDQVN 826

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4287	100.0	826	1	US-08-785-241-6	Sequence 6, Appli
2	4287	100.0	826	2	US-08-480-473B-2	Sequence 2, Appli
3	4287	100.0	826	3	US-08-915-213-2	Sequence 2, Appli
4	4287	100.0	826	3	US-09-148-547-2	Sequence 2, Appli
5	4287	100.0	826	3	US-09-235-217-2	Sequence 2, Appli
6	4287	100.0	826	3	US-09-380-662-23	Sequence 23, Appl
7	4287	100.0	826	4	US-09-438-833-1	Sequence 1, Appli
8	4287	100.0	826	4	US-09-702-705-330	Sequence 330, App
9	4287	100.0	826	4	US-09-736-457-330	Sequence 330, App
10	4287	100.0	826	4	US-09-383-581-2	Sequence 2, Appli
11	4287	100.0	826	4	US-09-614-124B-330	Sequence 330, App
12	4287	100.0	826	4	US-09-671-325-330	Sequence 330, App
13	4287	100.0	826	4	US-09-589-184-330	Sequence 330, App
14	4287	100.0	826	4	US-09-658-824-330	Sequence 330, App
15	4287	100.0	826	4	US-09-959-873B-18	Sequence 18, Appl
16	4287	100.0	826	4	US-09-949-016-6089	Sequence 6089, Ap
17	4287	100.0	826	4	US-09-967-388-4	Sequence 4, Appli

					us-09-922-958-4.ra	
18	4287	100.0	826	5	PCT-US96-10251-2	Sequence 2, Appli
19	4273.5	99.7	827	4	US-09-919-039-149	Sequence 149, App
20	4224	98.5	813	4	US-09-438-833-12	Sequence 12, Appl
21	4156	96.9	805	2	US-08-480-473B-4	Sequence 4, Appli
22	4156	96.9	805	3	US-08-915-213-4	Sequence 4, Appli
23	4156	96.9	805	3	US-09-235-217-4	Sequence 4, Appli
24	4156	96.9	805	5	PCT-US96-10251-4	Sequence 4, Appli
25	3939	91.9	756	4	US-09-438-833-11	Sequence 11, Appl
26	3751	87.5	810	1	US-08-785-241-7	Sequence 7, Appli
27	3404	79.4	652	4	US-09-438-833-5	Sequence 5, Appli
28	3135.5	73.1	623	4	US-09-967-388-2	Sequence 2, Appli
29	3021.5	70.5	613	4	US-09-438-833-6	Sequence 6, Appli
30	2715	63.3	532	4	US-09-949-016-7389	Sequence 7389, Ap
31	1942	45.3	373	2	US-08-480-473B-3	Sequence 3, Appli
32	1942	45.3	373	3	US-08-915-213-3	Sequence 3, Appli
33	1942	45.3	373	3	US-09-235-217-3	Sequence 3, Appli
34	1942	45.3	373	5	PCT-US96-10251-3	Sequence 3, Appli
35	1764.5	41.2	870	1	US-08-785-241-4	Sequence 4, Appli
36	1764.5	41.2	870	3	US-09-374-454-6	Sequence 6, Appli
37	1762	41.1	330	4	US-09-438-833-4	Sequence 4, Appli
38	1720	40.1	875	1	US-08-785-241-5	Sequence 5, Appli
39	1579	36.8	311	4	US-09-438-833-7	Sequence 7, Appli
40	1522	35.5	301	4	US-09-438-833-10	Sequence 10, Appl
41	1459	34.0	288	4	US-09-438-833-9	Sequence 9, Appli
42	1458	34.0	485	3	US-09-374-454-4	Sequence 4, Appli
43	1301	30.3	245	4	US-09-438-833-3	Sequence 3, Appli
44	1165	27.2	238	4	US-09-949-016-9161	Sequence 9161, Ap
45	896	20.9	1507	4	US-09-914-259-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1

US-08-785-241-6

; Sequence 6, Application US/08785241

; Patent No. 5695963

; GENERAL INFORMATION:

; APPLICANT: McKnight, Steven L.

; APPLICANT: Russell, David W.

; APPLICANT: Tian, Hui

; TITLE OF INVENTION: Endothelial PAS Domain Protein

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/785,241

; FILING DATE: 17-JAN-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: OSMAN, RICHARD A

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: UTSD:1229


```

: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 343-4341
: TELEFAX: (415) 343-4342
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 826 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-785-241-6

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Query Match          100.0%; Score 4287; DB 1; Length 826;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 826; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEGAGGANDKKKISSERRKEKSRDAARSRRSKESEVFYELAHQLPLPHNVSSHLDKASVM 60
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Db      1 MEGAGGANDKKKISSERRKEKSRDAARSRRSKESEVFYELAHQLPLPHNVSSHLDKASVM 60

Qy     61 RLTISYLRVRKLLDAGDLIEDDMKAQMNC FYLKALDGFVMVL TDDGDMIYISDNVNKYM 120
      |||
Db     61 RLTISYLRVRKLLDAGDLIEDDMKAQMNC FYLKALDGFVMVL TDDGDMIYISDNVNKYM 120

Qy    121 GLTQFELTGHSVDFDTHPCDHEEMREMLTHRNLVKKGKEQNTQRSFFLRMKCTLTSRGR 180
      |||
Db    121 GLTQFELTGHSVDFDTHPCDHEEMREMLTHRNLVKKGKEQNTQRSFFLRMKCTLTSRGR 180

Qy    181 TMNIKSATWKVLHCTGHIHVYDTNSNQPCGYKKPPMTCLVLICEPIPHPSNIEIPLDSK 240
      |||
Db    181 TMNIKSATWKVLHCTGHIHVYDTNSNQPCGYKKPPMTCLVLICEPIPHPSNIEIPLDSK 240

Qy    241 TFLSRHSLDMKFSYCDERITELMGYEPEELLGRSIYEYYHALDS DHLTKTHDMFTKGQV 300
      |||
Db    241 TFLSRHSLDMKFSYCDERITELMGYEPEELLGRSIYEYYHALDS DHLTKTHDMFTKGQV 300

Qy    301 TTGQYRMLAKRGGYVWVETQATVIYNTKNSQPQCIVCVNYVSGIIQHDLIFSLQQTECV 360
      |||
Db    301 TTGQYRMLAKRGGYVWVETQATVIYNTKNSQPQCIVCVNYVSGIIQHDLIFSLQQTECV 360

Qy    361 LKPVESSDMKMTQLFTKVESED TSSLFDKLKKEPDALTLLAPAAGDTIISLDFGSNDTET 420
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Db    361 LKPVESSDMKMTQLFTKVESED TSSLFDKLKKEPDALTLLAPAAGDTIISLDFGSNDTET 420

Qy    421 DDQQL EEVPLYNDVMLPSPNEKLQINLAMSPLPTAETPKPLRSSADPALNQEVALKLEP 480
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Db    421 DDQQL EEVPLYNDVMLPSPNEKLQINLAMSPLPTAETPKPLRSSADPALNQEVALKLEP 480

Qy    481 NPESLELSFTMPQIQDQTPSPSDGSTRQSSPEPNPSEYCFYVDS DMVNEFKLELVEKLF 540
      |||
Db    481 NPESLELSFTMPQIQDQTPSPSDGSTRQSSPEPNPSEYCFYVDS DMVNEFKLELVEKLF 540

Qy    541 AEDTEAKNPFSTQD TDLDLEMLAPYIPMDDDFQLRSFDQLSPLESSSASPESASPQSTVT 600
      |||
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Qy    601 VFQQTQIQEPTANATTTTATTD ELKTVTKDRMEDIKILIASPSPTHIHKETTSATSSPYR 660
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Db    601 VFQQTQIQEPTANATTTTATTD ELKTVTKDRMEDIKILIASPSPTHIHKETTSATSSPYR 660

Qy    661 DTQSRTASPNRAGKGVIEQTEKSHPRSPNVLSVALSQRTTVPEEELNPKILALQNAQRKR 720
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Db    661 DTQSRTASPNRAGKGVIEQTEKSHPRSPNVLSVALSQRTTVPEEELNPKILALQNAQRKR 720

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Qy 721 KMEHDGSLFQAVGIGTLLQQPDDHAATTSLSWKRVKGCKSSEQNGMEQKTIILIPSDLAC 780
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 Db 721 KMEHDGSLFQAVGIGTLLQQPDDHAATTSLSWKRVKGCKSSEQNGMEQKTIILIPSDLAC 780
 Qy 781 RLLGQSMDESGLPQLTSYDCEVNAPIQGSRNLLQGEELLRALDQVN 826
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 Db 781 RLLGQSMDESGLPQLTSYDCEVNAPIQGSRNLLQGEELLRALDQVN 826

RESULT 2

US-08-480-473B-2

; Sequence 2, Application US/08480473B

; Patent No. 5882914

GENERAL INFORMATION:

; APPLICANT: Semenza, Gregg L.

; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE

; NUMBER OF SEQUENCES: 64

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 4225 Executive Square, Suite 1400

; CITY: La Jolla

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/480,473B

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Haile, Lisa A.

; REGISTRATION NUMBER: 38,347

; REFERENCE/DOCKET NUMBER: 07265/053001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619/678-5070

; TELEFAX: 619/678-5099

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 826 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-480-473B-2

Query Match 100.0%; Score 4287; DB 2; Length 826;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 826; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEGAGGANDKKKISSERRKEKSRDAARSRRSKESEVFYELAHQLPLPHNVSSHLDKASVM 60
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 Db 1 MEGAGGANDKKKISSERRKEKSRDAARSRRSKESEVFYELAHQLPLPHNVSSHLDKASVM 60
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 Db 61 RLTISYLRVRKLLDAGDLIEDDMKAQMNC FYLKALDGFVMVLTDDGDMIIYISDNVNKYM 120
 Qy 121 GLTQFELTGHSVFDFTHPCDHEEMREMLTHRNGLVKKGKEQNTQRSFFLRMCKTLTSRGR 180
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us-09-922-958-4.ra1

Db 121 GLTQFELTGHSVDFDTHPCDHEEMREMLTHRNLVKKGKEQNTQRSFFLRMKCTLTSGRGR 180
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 Db 181 TMNIKSATWKVLHCTGHIHVYDTNSNQPCGYKKPPMTCLVLICEPIPHPSNIEIPLDSK 240
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 Db 301 TTGQYRMLAKRGGYVWVETQATVIYNTKNSQPQCIVCVNYVVSIGIIQHDLIFSLQQTECV 360
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 Db 361 LKPVESDMKMTQLFTKVESEDSSSLFDKLLKEPDALTLLAPAAGDTIISLDFGSNDTET 420
 Qy 421 DDQQL EEVPLYNDVMLPSPNEKLQINLAMSPLPTAETPKPLRSSADPALNQEVALKLEP 480
 Db 421 DDQQL EEVPLYNDVMLPSPNEKLQINLAMSPLPTAETPKPLRSSADPALNQEVALKLEP 480
 Qy 481 NPESLELSFTMPQIQDQTPSPSDGSTRQSSPEPNPSEYCFYVDSMDVNEFKLELVEKLF 540
 Db 481 NPESLELSFTMPQIQDQTPSPSDGSTRQSSPEPNPSEYCFYVDSMDVNEFKLELVEKLF 540
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 Db 541 AEDTEAKNPFSTQDQDLDLEMLAPYIPMDDDFQLRSFDQLSPLESSSASPESASPQSTVT 600
 Qy 601 VFQQTQIQEPTANATTTTATTDDELKTVTKDRMEDIKILIASPSPTHIHKETTSATSSPYR 660
 Db 601 VFQQTQIQEPTANATTTTATTDDELKTVTKDRMEDIKILIASPSPTHIHKETTSATSSPYR 660
 Qy 661 DTQSRTASPNRAGKGVIEQTEKSHPRSPNVLSVALSQRTTVPEEELNPKILALQNAQRKR 720
 Db 661 DTQSRTASPNRAGKGVIEQTEKSHPRSPNVLSVALSQRTTVPEEELNPKILALQNAQRKR 720
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 Db 721 KMEHDGSLFQAVGIGTLLQQPDDHAATTSLSWKRVKGCKSSEQNGMEQKTIILIPSDLAC 780
 Qy 781 RLLGQSMDESGLPQLTSYDCEVNAPIQGSRNLLQGEELLRALDQVN 826
 Db 781 RLLGQSMDESGLPQLTSYDCEVNAPIQGSRNLLQGEELLRALDQVN 826

us-09-922-958-5.ra1

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OM protein - protein search, using sw model

Run on: July 27, 2005, 07:43:11 ; Search time 3.68182 Seconds
(without alignments)
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Title: US-09-922-958-5
Perfect score: 275
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	275	100.0	116	4	US-09-438-833-8	Sequence 8, Appli
2	275	100.0	288	4	US-09-438-833-9	Sequence 9, Appli
3	275	100.0	301	4	US-09-438-833-10	Sequence 10, Appl
4	275	100.0	311	4	US-09-438-833-7	Sequence 7, Appli
5	275	100.0	532	4	US-09-949-016-7389	Sequence 7389, Ap
6	275	100.0	613	4	US-09-438-833-6	Sequence 6, Appli
7	275	100.0	652	4	US-09-438-833-5	Sequence 5, Appli
8	275	100.0	756	4	US-09-438-833-11	Sequence 11, Appl
9	275	100.0	805	2	US-08-480-473B-4	Sequence 4, Appli
10	275	100.0	805	3	US-08-915-213-4	Sequence 4, Appli
11	275	100.0	805	3	US-09-235-217-4	Sequence 4, Appli
12	275	100.0	805	5	PCT-US96-10251-4	Sequence 4, Appli
13	275	100.0	810	1	US-08-785-241-7	Sequence 7, Appli
14	275	100.0	813	4	US-09-438-833-12	Sequence 12, Appl
15	275	100.0	826	1	US-08-785-241-6	Sequence 6, Appli
16	275	100.0	826	2	US-08-480-473B-2	Sequence 2, Appli
17	275	100.0	826	3	US-08-915-213-2	Sequence 2, Appli

				us-09-922-958-5.ra		
18	275	100.0	826	3	US-09-148-547-2	Sequence 2, Appli
19	275	100.0	826	3	US-09-235-217-2	Sequence 2, Appli
20	275	100.0	826	3	US-09-380-662-23	Sequence 23, Appl
21	275	100.0	826	4	US-09-438-833-1	Sequence 1, Appli
22	275	100.0	826	4	US-09-702-705-330	Sequence 330, App
23	275	100.0	826	4	US-09-736-457-330	Sequence 330, App
24	275	100.0	826	4	US-09-383-581-2	Sequence 2, Appli
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27	275	100.0	826	4	US-09-589-184-330	Sequence 330, App
28	275	100.0	826	4	US-09-658-824-330	Sequence 330, App
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42	64.5	23.5	143	4	US-09-270-767-42631	Sequence 42631, A
43	64.5	23.5	1507	4	US-09-914-259-37	Sequence 37, Appl
44	63	22.9	440	4	US-09-538-092-1264	Sequence 1264, Ap
45	62	22.5	335	4	US-09-328-352-7832	Sequence 7832, Ap

ALIGNMENTS

RESULT 1

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US-09-438-833-8
; Sequence 8, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: Protein variants
; FILE REFERENCE: 1848
; CURRENT APPLICATION NUMBER: US/09/438,833
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Subdomain
; OTHER INFORMATION: 526-641 of human HIF-1 alpha
US-09-438-833-8

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Query Match          100.0%; Score 275; DB 4; Length 116;
Best Local Similarity 100.0%; Pred. No. 2.5e-30;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      7 KLELVEKLF AEDTEAKNPFSTQD TDL DLEMLAPYIPMDDDFQLRSFDQLSPLES 60

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RESULT 2

US-09-438-833-9

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; Sequence 9, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
;   APPLICANT: Pharmacia & Upjohn
;   TITLE OF INVENTION: Protein variants
;   FILE REFERENCE: 1848
;   CURRENT APPLICATION NUMBER: US/09/438,833
;   CURRENT FILING DATE: 1999-11-12
;   NUMBER OF SEQ ID NOS: 15
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 288
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Subdomain
;   OTHER INFORMATION: 526-813 of human HIF-1 alpha
US-09-438-833-9
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Best Local Similarity 100.0%; Pred. No. 8.1e-30;
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RESULT 3

US-09-438-833-10

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; Sequence 10, Application US/09438833
; Patent No. 6436654
; GENERAL INFORMATION:
;   APPLICANT: Pharmacia & Upjohn
;   TITLE OF INVENTION: Protein variants
;   FILE REFERENCE: 1848
;   CURRENT APPLICATION NUMBER: US/09/438,833
;   CURRENT FILING DATE: 1999-11-12
;   NUMBER OF SEQ ID NOS: 15
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 301
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Subdomain
;   OTHER INFORMATION: 526-826 of human HIF-1 alpha
US-09-438-833-10
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Query Match          100.0%; Score 275; DB 4; Length 301;
Best Local Similarity 100.0%; Pred. No. 8.6e-30;
Matches    54; Conservative    0; Mismatches    0; Indels    0; Gaps    0;
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Db      7 KLELVEKLFAEDTEAKNPFSTQDLDLEMLAPYIPMDDDFQLRSFDQLSPLES 60
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